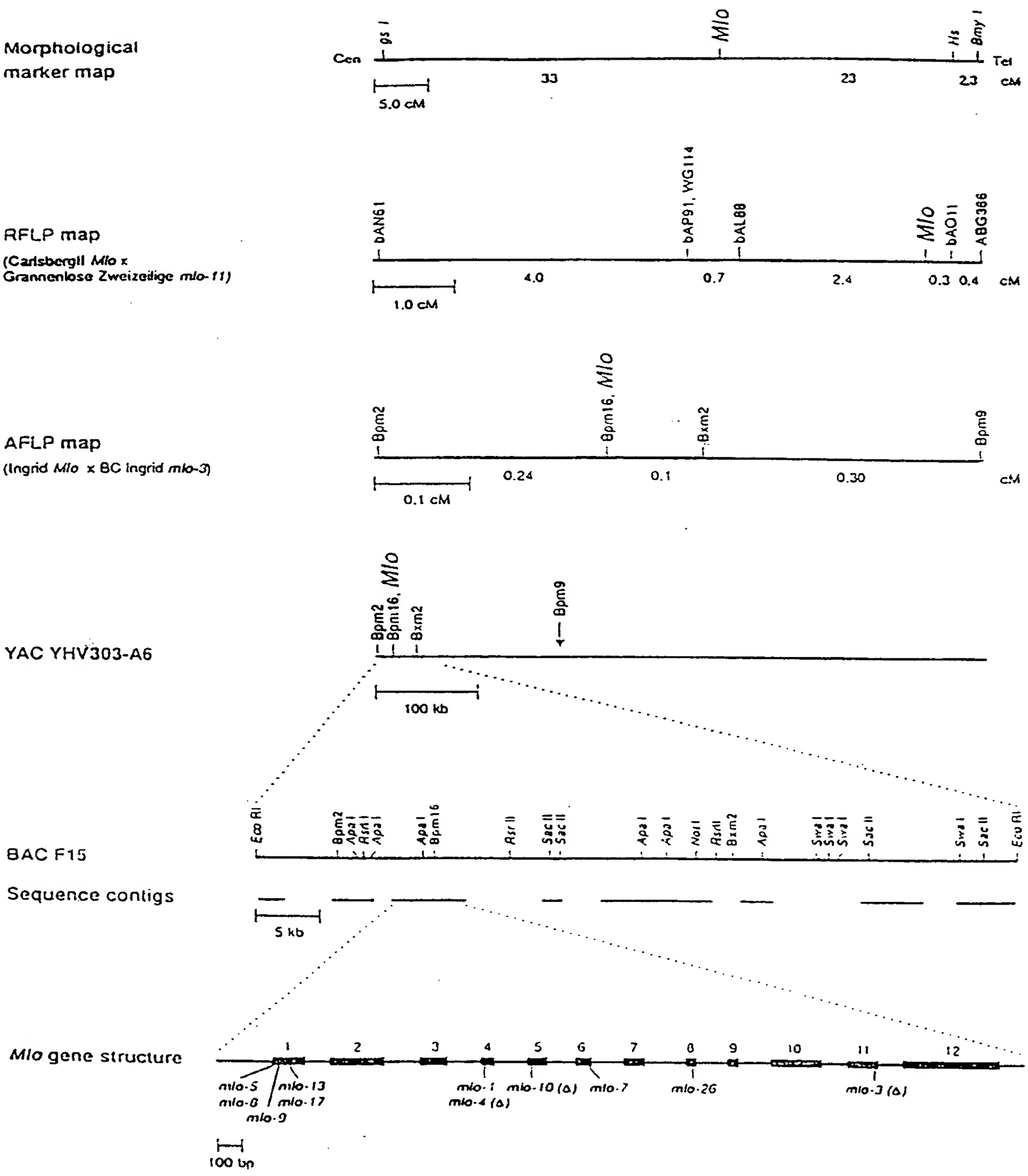
Morphological marker map
Cen
gs 1
Mlo
His
Bmy 1
Tel
33
23
23
cM
5.0 cM
RFLP map
(Carlsbergll Mlo x Grannenlose Zweizeilige mlo-11)
bAN61
bAP91, WG114
bAL88
Mlo
bAO11
ABG386
4.0
0.7
2.4
0.3
0.4
cM
1.0 cM
AFLP map
(Ingrid Mlo x BC Ingrid mlo-3)
Bpm2
Bpm16, Mlo
Bxm2
Bpm9
0.24
0.1
0.30
cM
0.1 cM
YAC YHV303-A6
Bpm2
Bpm16, Mlo
Bxm2
Bpm9
100 kb
BAC F15
Eco RI
Bpm2
Apa I
Asn I
Apa I
Apa I
Bpm16
Asr II
Sac II
Sac II
Apa I
Apa I
Not I
Asn II
Bxm2
Apa I
Sma I
Sma I
Sma I
Sac II
Sma I
Sac II
Eco RI
Sequence contigs
5 kb
Mlo gene structure
1
2
3
4
5
6
7
8
9
10
11
12
mlo-5
mlo-8
mlo-9
mlo-13
mlo-17
mlo-1
mlo-4 (Δ)
mlo-10 (Δ)
mlo-7
mlo-26
mlo-3 (Δ)
100 bp

Figure 1

```
 M  S  D  K  K  G  V  P  A  R  E  L  P  E  T  P  S  W  A  V
ATGTCGGACAAAAAAGGGGTGCCGGCGCGGGAGCTGCCGGAGACGCCGTCGTGGGCGGTG      60

 A  V  V  F  A  A  M  V  L  V  S  V  L  M  E  H  G  L  H  K
GCGGTGGTCTTCGCCGCCATGGTGCTCGTGTCCGTCCTCATGGAACACGGCCTCCACAAG     120

 L  G  H  W  F  Q  H  R  H  K  K  A  L  W  E  A  L  E  K  M
CTCGGCCATTGGTTCCAGCACCGGCACAAGAAGGCCCTGTGGGAGGCGCTGGAGAAGATG     180

 K  A  E  L  M  L  V  G  F  I  S  L  L  L  I  V  T  Q  D  P
AAGGCGGAGCTCATGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGACCCC     240

 I  I  A  K  I  C  I  S  E  D  A  A  D  V  M  W  P  C  K  R
ATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTCATGTGGCCCTGCAAGCGC     300

 G  T  E  G  R  K  P  S  K  Y  V  D  Y  C  P  E  G  K  V  A
GGCACCGAGGGCCGCAAGCCCAGCAAGTACGTTGACTACTGCCCGGAGGGCAAGGTGGCG     360

 L  M  S  T  G  S  L  H  Q  L  H  V  F  I  F  V  L  A  V  F
CTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTCTTCATCTTCGTGCTCGCGGTCTTC     420

 H  V  T  Y  S  V  I  T  I  A  L  S  R  L  K  M  R  T  W  K
CATGTCACCTACAGCGTCATCACCATAGCTCTAAGCCGTCTCAAAATGAGAACATGGAAG     480

 K  W  E  T  E  T  T  S  L  E  Y  Q  F  A  N  D  P  A  R  F
AAATGGGAGACAGAGACCACCTCCTTGGAATACCAGTTCGCAAATGATCCTGCACGGTTC     540

 R  F  T  H  Q  T  S  F  V  K  R  H  L  G  L  S  S  T  P  G
CGGTTCACGCACCAGACGTCGTTCGTGAAGCGCCACCTGGGCCTCTCCAGCACCCCTGGC     600

 I  R  W  V  V  A  F  F  R  Q  F  F  R  S  V  T  K  V  D  Y
ATCAGATGGGTGGTGGCCTTCTTCAGGCAGTTCTTCAGGTCAGTCACCAAGGTGGACTAC     660

 L  T  L  R  A  G  F  I  N  A  H  L  S  Q  N  S  K  F  D  F
CTGACCTTGAGGGCAGGCTTCATCAACGCGCATTTGTCGCAAAACAGCAAGTTCGACTTC     720

 H  K  Y  I  K  R  S  M  E  D  D  F  K  V  V  V  G  I  S  L
CACAAGTACATCAAGAGGTCGATGGAGGACGACTTCAAGGTCGTCGTCGGCATCAGCCTC     780

 P  L  W  G  V  A  I  L  T  L  F  L  D  I  N  G  V  G  T  L
CCGCTGTGGGGTGTGGCGATCCTCACCCTCTTCCTTGACATCAATGGGGTTGGCACGCTC     840

 I  W  I  S  F  I  P  L  V  I  L  L  C  V  G  T  K  L  E  M
ATCTGGATTTCTTTCATCCCTCTCGTGATCCTCTTGTGTGTTGGAACCAAGCTGGAGATG     900

 I  I  M  E  M  A  L  E  I  Q  D  R  A  S  V  I  K  G  A  P
ATCATCATGGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCGTCATCAAGGGGGCCCCC     960

 V  V  E  P  S  N  K  F  F  W  F  H  R  P  D  W  V  L  F  F
GTGGTCGAGCCCAGCAACAAGTTCTTCTGGTTCCACCGCCCCGACTGGGTCCTCTTCTTC    1020

 I  H  L  T  L  F  Q  N  A  F  Q  M  A  H  F  V  W  T  V  A
ATACACCTGACGTTGTTCCAGAACGCGTTTCAGATGGCGCATTTTGTGTGGACAGTGGCC    1080

 T  P  G  L  K  K  C  Y  H  T  Q  I  G  L  S  I  M  K  V  V
ACGCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGGCTGAGCATCATGAAGGTGGTG    1140

 V  G  L  A  L  Q  F  L  C  S  Y  M  T  F  P  L  Y  A  L  V
GTGGGGCTAGCTCTCCAGTTCCTCTGCAGCTATATGACCTTCCCCCTCTACGCGCTCGTC    1200

 T  Q  M  G  S  N  M  K  R  S  I  F  D  E  Q  T  S  K  A  L
ACACAGATGGGATCAAACATGAAGAGGTCCATCTTCGACGAGCAGACGTCCAAGGCGCTC    1260

 T  N  W  R  N  T  A  K  E  K  K  K  V  R  D  T  D  M  L  M
ACCAACTGGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATGCTGATG    1320

 A  Q  M  I  G  D  A  T  P  S  R  G  S  S  P  M  P  S  R  G
GCTCAGATGATCGGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATGCCGAGCCGGGGC    1380
```

Figure 2

Figure 2 (Continued)

```
 S  S  P  V  H  L  L  H  K  G  M  G  R  S  D  D  P  Q  S  A
TCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGACCCCCAGAGCGCG     1440

 P  T  S  P  R  T  Q  Q  E  A  R  D  M  Y  P  V  V  V  A  H
CCCACCTCGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGGTTGTGGTGGCGCAC     1500

 P  V  H  R  L  N  P  N  D  R  R  R  S  A  S  S  S  A  L  E
CCGGTGCACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTCGTCGTCGGCCCTCGAA     1560

 A  D  I  P  S  A  D  F  S  F  S  Q  G  *
GCCGACATCCCCAGTGCAGATTTTTCCTTCAGCCAGGGATGA     1602
```

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Figure 3

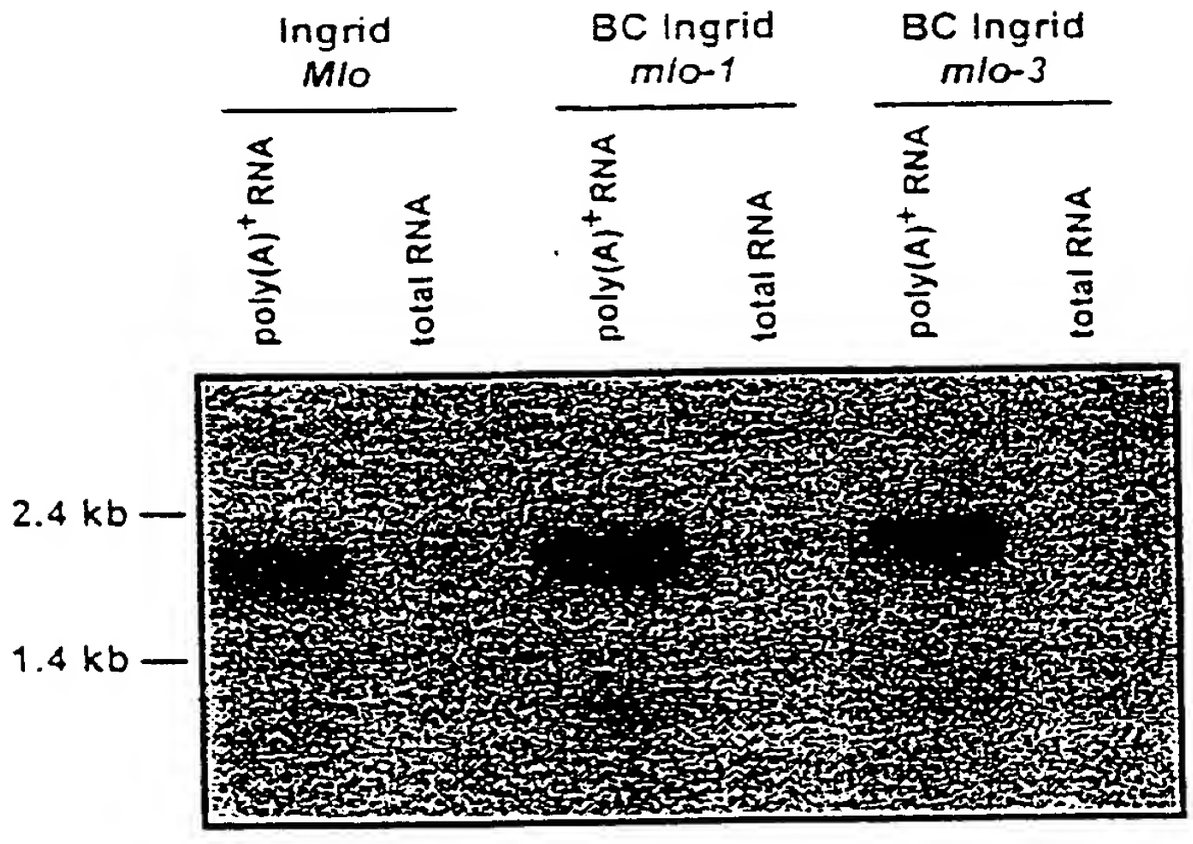

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Figure 4

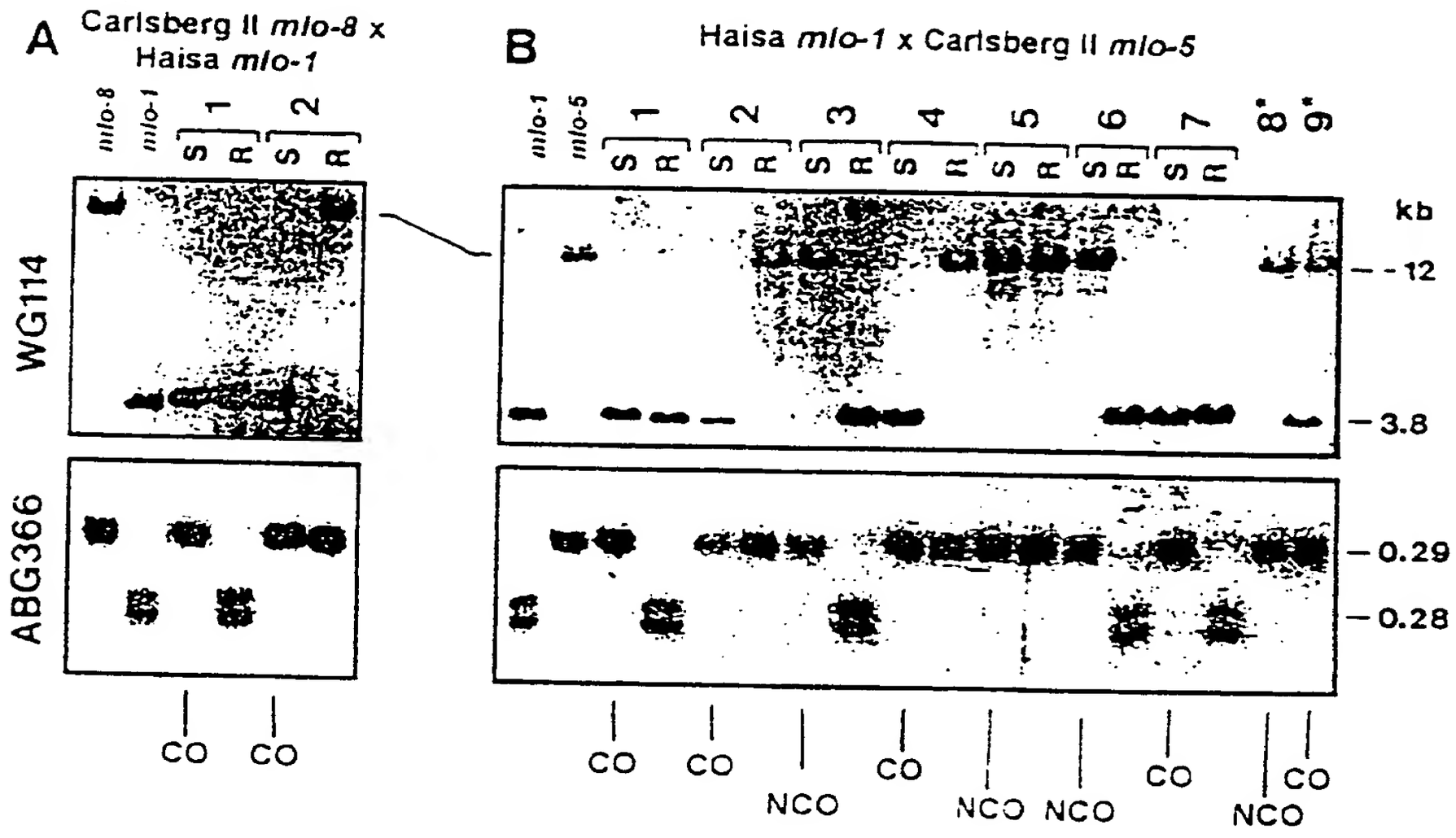

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FIGURE 5

```
292 GCGGAGCTCATGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCA 341
    || :|||| |||||| ||||||||||:|||||||| |||| ||| | ||
 80 GCANAGCTGATGCTGCTGGGCTTCATNTCCCTGCTTCTCACCGTGGCACA 129

342 GGACCCCATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTCA 391
    ||  ||   |||| |||:|| |||||| || ||   || ||| || ||
130 GGCGCC...CATCTCCAANATCTGCATCCCCAAGTCGGCTGCCAACATCT 176

392 TGTGGCCCTGCAAGCGCGGCACCGAGGGCCGC.AAGCCCAGCAAGTACGT 440
    ||| ||| ||||||   ||| : || | |  | |||  :|   || | ||
177 TGTTGCCGTGCAAGGCAGGCCNAGATGCCATCGAAGAANAAGCAGCAAGT 226

441 TGACTACTGCCCGGAGGTGAGCAGCAGAGCCCGGACCAGCAGCTTCACGA 490
     | |: |:| ||   ||   ||  | | | | ||  |  | ||| :|
227 GGTCNCCNGTCC.TTGGCCGGCGCCGGCGGCGGGGACTACTGCTCNAAAT 275

491 TGATGAAGAAATCAATACC.....GAACTTTTTCTTGTTTTCT 528
    |    || |  || :||          | ||    ||  : : :
276 TCGATGTGAGAATAACNCCAGCTGCCGGCAAGCACAACCTCGATNCNATN 325

529 TCTGATTGTCGTCTTGGCTTGGCTTAATTGGTGTGTGTGTGTGTTTGC 578
    ||:|||          |    |||||| | | | |  |  | | |||
326 ACTNATT.....TAACTATAATTGATTTTTCTTGGGTTTTCTGC 364

579 AGGGCAAGGTGGCGCTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTC 628
    |||||||||||||||| |||||  |   ||| ||||||||||||||| |
365 AGGGCAAGGTGGCGCTGATGTCGGCAAAGAGCATGCACCAGCTGCACATT 414

629 TTCATCTTCGTGCTCGCGGTCTTCCATGTCACCTACAGCGTCATCACCAT 678
    |||||||||||||||| || |||||||| |||||| || ||||||||||
415 TTCATCTTCGTGCTCGCCGTGTTCCATGTTACCTACTGCATCATCACCAT 464

579 AGCTCTAAGCCGTCTCAAAGTGAGCCTTTGCTTCT.....TCTTCTTCTT 723
     | | || | || ||||||||||  | |  ||||      || |   | |
465 GGGTTTAGGGCGCCTCAAAGTGAGTTTGTCGTTCTGTCCCTCATGCACAT 514

724 CTTTTACC........GCACGTCTGTCTGTCAGGCGTACCTACCTGTTCA 765
    ||||  |         ||| :  |||| |||   |  |   |    |||
515 GTTTTCTCTAGTTCTAGCAANATTGTCAGTCCTTCAAATGGATTGTTTCG 564

766 TCAGGCTTGAGTAAAACTGTTCCATAATCTGC.........TCCGGCATAA 807
    ||       || ||  |  ||   |||| |||          |    ||||
565 ACA......AGAAACCCAATTTATTAATTTGCCAGTTAAATATATAATAA 608

808 TCCTCTCCTCCTG....CAGATGAGAACATGGAAGAAATGGGAGACAGAG 853
    |       || ||     |||||| | |||||||| |||||| || ||
609 TTGATCTTTCTTGGTTTTAGATGAAGAAATGGAAGAAGTGGGAGTCACAG 658

854 ACCACCTCCTTGGAATACCAGTTCGCAAATGGTCAGGATCCCCCACTCTG 903
    |||| ||| ||||| || |||||||||| |||   |       | |
659 ACCAACTCATTGGAGTATCAGTTCGCAATCGGTAGTG.......AATTAA 701

904 CAATCTCCC...CTTCTTCGAAACCAAACC....TGATGATCCATTTAAA 946
     ||||||||   ||  |||    |  ||||    |||| ||   || |||
702 GAATCTCCCTAACTATTTCATTTCAGAACCTTTATGATAATGTCTTGAAA 751

947 GACGCAGGCACGATCAGAGTGAGTGAACTGATGTATGTTCATTTTTTGTG 996
    || |  |      |||||  |||   |  ||||  |
752 GAGGAGGAGCAAATCAG.CTGAAAAATATGATCGA.............. 785

997 TCCTTTCAGATCCTGCACGGTTCCGGTTCACGCACCAGACGTCGTTCGTG 1046
    ||| | |||||||| |||| ||| |||||||||| ||||||||||||||
786 TCCATGCAGATCCTTCACGATTCAGGTTCACGCATCAGACGTCGTTCGTG 835
```

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FIGURE 5 c nt'd


```
1047 AAGCGCCACCTGGG...CCTCTCCAGCACCCCTGGCATCAGATGGGTGGT 1093
     ||||| || ||||||     |||| ||||||||||||  |||||||| | ||
 836 AAGCGGCATCTGGGATCATTCTCAAGCACCCCTGGGCTCAGATGGATCGT 885

1094 GAGTTTTTTAGCTTCTTATCTGCCCCTCATCTGTGTGTAATGTT..... 1137
     ||||| |  | || |  ||         |||  ||| |  | ||
 886 GAGTTATCAATCTCCGAAT.......ACATGCTTGTTTTTTATTCTTGCA 928

1138 ..TGGCGTA..........TGGAGTCAGGTGATTT.........ACCTT 1165
       ||||  ||           |  |  ||  |  |||         |  |
 929 ACTGGCCTAGCTGTTCCAATTCAATCCATATTTTTTGAAAAAAAAAATAT 978

1166 GCCTGTGATGTTTGTTGCCTTGTCAGGTGGCCTTCTTCAGGCAGTTCTTC 1215
      | ||   ||||||     ||||  ||||  || ||||||||||||||||
 979 TCATGCCGTGTTTG.....TTGTTAGGTAGCATTCTTCAGGCAGTTCTTT 1023

1216 AGGTCAGTCACCAAGGTGGACTACCTGACCTTGAGGGCAGGCTTCATCAA 1265
     |||| ||||||||||||||||||||||||| || ||  ||||||||||||
1024 GGGTCCGTCACCAAGGTGGACTACCTGACCATGCGGCAAGGCTTCATCAA 1073

1266 CGTACGTGC....CTCCCCTTCTAGCTCCGCCATTGCTGCCGCGATGTAG 1311
      |||  | |    |  |||       | |  ||||| ||  ||  |  ||
1074 TGTATATACTAATCAAACCTGACCAATTCAACATTGATGATGC.AAACAG 1122

1312 CAGCAAAGCTTCT.......CAAGTTATCCTTCTGACGCTAAAGTTCCCA 1354
      ||   || || |        | |||| | | | ||| | ||| |
1123 AAGACCAGGTTTTTTTTTCCGAGTTGTGCAT.TGAAGTTAATG...... 1165

1355 TGTTTTTTCCTCAAATTATTCTGCGCAGGCG.CATTTGTCGCAAAACAGC 1403
      |||||  | ||  || |  | |||||| ||||||||||  || |||
1166 .GTTTTAGCTTC...TTCTCTTTTGCAGGCGCCATTTGTCGCAGAATAGC 1211

1404 AAGTTCGACTTCCACAAGTACATCAAGAGGTCGATGGAGGACGACTTCAA 1453
     |||||||||||||||| |||||||||||||  ||||||||||||||||
1212 AAGTTCGACTTCCACAAATACATCAAGAGGTCTTTGGAGGACGACTTCAA 1261

1454 GGTCGTCGTCGGCATCAGGTACGTTCCATTCCTTCCTCTGCACCAGACCA 1503
      || |||||  ||||||||||  ||       ||||  ||  |
1262 AGTTGTCGTTGGCATCAGGTCCG......TCCTCGCTTT..... 1294

1504 CACCCCATGGATAGATTTTAACAATTGCTGTCAGGTTCCACATGATAACA 1553
               ||  |||  ||  |    ||  |  |  |||  ||||  |
1295 ..........ATTAATTATAGGA....CTCTTATATTCAACATTTTTTTT 1330

1554 ATATACTATGA.ACTTGGTCTTTGCTCCTTGTCCTTG.....CACGATCA 1597
      |||  |  |  | | ||  ||||   |  ||||  ||         ||||
1331 ATAAAGAAACATATTTAGTCT...CCAGTTGTGTATGTGTATGTGGATCT 1377

1598 TGACACATTTGGCCTGTTTTCGCAGCCTCCCGCTGTGGGGTGTGGCGATC 1647
     |||||||||||| ||| ||| |||||||||| ||||||   ||  |  |||
1378 TGACACATTTGG.CTGGTTTTGCAGCCTCCCTCTGTGGTTCGTCGGAATC 1426

1648 CTCACCCTCTTCCTTGACATCAATGGTATGGACCTTCTCCTCTCCGGTTT 1697
      ||    |||||||| || ||| | ||||    |||| ||||       |||
1427 CTTGTACTCTTCCTCGATATCCACGGTA..ATCCTTGTCCT.....ATTT 1469

1698 CTCTATTGCTTTGCAGCTAAATAAAACACTTGCAATTCGTCTCGTGATCA 1747
     |  | ||  |||    || || |       |  |||| |||| | ||||
1470 CATTCTTTTTTTACTCTCAAAACCTTGTTCTGAATTGGTCTTATAATCA 1519

1748 CCGCTCATTTTTCAACCATTTCTTTTTCTACTCATAGGGGTTGGCACGCT 1797
      ||    ||||||   | | || |||  |  |   ||||  |||||||  ||
1520 CCATCGATTTTTTTTCAACTT.TTTCCCCGCGTGTAGGTCTTGGCACACT 1568

1798 CATCTGGATTTCTTTCATCCCTCTCGTGGTAAGTGC.AGATTTCTCC.AT 1845
      || ||||| |||||  | |||||| | ||||| || | |||||  ||  |
1569 TATTTGGATCTCTTTTGTTCCTCTCATCGTAAGAGCGAAATTTCCCCTGT 1618
```

FIGURE 5 cont'd

```
1846 CGAAAGCAACAGCAAACCCAATT.....TGATCGCAAT 1878
     | ||||  |||||  |||  ||||          | ||  |||
1619 CCAAAGAAACAGTTAACATAATTAATTATGCTTTAATTTATCATGAAAAT 1668

1879 GGAAACCCACACCTAATATTAACTCAAAATGTCAATTGTCGGTGCGTCTT 1928
       | |    ||  |||        ||||  |||  |||  |||  |
1669 TAATATGATCATATAACTAATGAACAAACATTCA..TGTGAATGCCACCG 1716

1929 CCTCAACAGATCCTCTTGTGTGTTGGAACCAAGCTGGAGATGATCATCAT 1978
          ||||||  ||||||  |||||  |||||||  ||||||  | |||||
1717 TTGTCTCAGATCGTCTTGTTAGTTGGGACCAAGCTAGAGATGGTGATCAT 1766

1979 GGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCGTCATCAAGGGGGCCC 2028
     ||||||||||  |||||  ||||||  ||||  |  ||  |||  ||||  ||  |
1767 GGAGATGGCCCAAGAGATACAGGACAGGGCCACTGTGATCCAGGGAGCAC 1816

2029 CCGTGGTCGAGCCCAGCAACAAGTTCTTCTGGTTCCACCGCCCCGACTGG 2078
     |  ||||  ||  ||  ||||||||||  ||||||||||  |||||||  ||||||
1817 CTATGGTTGAACCAAGCAACAAGTACTTCTGGTTCAACCGCCCTGACTGG 1866

2079 GTCCTCTTCTTCATACACCTGACGTTGTT..................... 2107
     |||  |  ||||||||||||||||||  |  ||
1867 GTCTTGTTCTTCATACACCTGACACTCTTCCCATGTACATGTTTAAAACC 1916

                                    .
                                    .
                                    .

2108 .....CCAGAACGC.GTTTCAGATGGCGCATTTTG 2136
                 |||||||||  ||||||||||||||||||  |
2017 GACGGACGGATCGATCATCACCAGAACGCATTTTCAGATGGCGCATTTCG 2066

2137 TGTGGACAGTG....GTACGCCAC.........CGATGAACTTGTCAGTT 2173
     | |||||  ||    |||  ||  ||          | ||   ||  ||||||
2067 TATGGACTATGGTGTGTATGCTACTTGCTTAGTTGTTGCCATTATCAGTT 2116

2174 .......AACATGGGTGTCA...AGGCACCGAGTGCCGCTGATGA..... 2208
            ||  |  ||||  |   |  ||||  ||       ||  ||||
2117 CTTAAGCAAATTAAGTGTGATGCATGCACTGA......CTAATGAGACAA 2160

2209 ........ACTGCTCTGACGGAGATTTACTTGTGTTGT.......AGGCC 2243
             ||  |||    |   |||  |  ||||  ||||        ||||
2161 AAAATGACACAGCTTGTTCATCGATCTGGTTGTTTTGTGTGTGACAGGCA 2210

2244 ACGCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGGCTGAGCATCAT 2293
     ||  ||  ||  ||||||||||||  |||      |  ||  ||||||||||||  |
2211 ACACCTGGTCTGAAGAAATGCTTCCATGAAAATATTTGGCTGAGCATCGT 2260

2294 GAAGGTGGTGGTGGGGCTAGCTCTCCAGTTCCTCTGCAGCTATATGACCT 2343
     |  |  ||  |  ||||||  |  ||||  |||  |  ||  ||||||||  ||  ||||
2261 GGAAGTCATTGTGGGGATCTCTCTTCAGGTGCTATGCAGCTACATCACCT 2310

2344 TCCCCCTCTACGCGCTCGTCACACAGGTAATAAAACCGTCCAGGAA 2389
     ||||  ||||||||||||||||||||||||  |  ||  ||  |  ||  ||
2311 TCCCGCTCTACGCGCTCGTCACACAGGTGAACAAGCCATTCACAAA 2356
```

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FIGURE 6

```
295 GAGCTCATGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGA 344
    ||||||:||||||||||||||||||||||||||||||||||||||||||||
  1 GAGCTCNTGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGA 50

345 CCCCATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTCATGT 394
    ||   | || ||| ||| |||||||||| |||| |||| |||:  :|||
 51 TCC...CGTCTCCAGGATCTGCATCTCCAAGGAGGCCGGCGANAANATGC 97

395 GGCCCTGCAAG.....CGCGGCACCGAGGGCCGCAAGCCCA..... 430
      || |||||||      : |||| |||  ||  ||||   ||
 98 TCCCGTGCAAGCCTTACNACGGCGCCGGCGGTGGCAAAGGCAATGACAAT 147

431 ..........................GCAAGTACGTTGACTACTGCCCGGA 455
                               || |:  ||  :  | || ||| |
148 CACCGGAGGCTTCTCTGGCTCCAAGGCGANAGCGANACCCACCGCCGGTT 197

456 GGTGAGCAGCAGAGCCCGGACCAG..... 479
      || ||  ||   | ||||||:  |
198 CCTG.GCTGCCCCGGCCGGANTGGACGTCTGCGCCAAACAGGTGAGCACC 246

480 CAGCTTCACGATGATGAAGAAA.TCAATACCGAACTTTTTCTTGTTTTCT 528
     |:| ||:| |   |    | ||| | : ||  || | |   | ||  ||
247 TANCGTCNCCACAAACCACAAACTANCTAATGAGCATGGACCTGAATTTC 296

529 TCTGATTGTCGTCTTGGCTTGGCTTAATTGGTGTGTGTGTGTGTGTTTGC 578
    |    || | | |||||||||| || |||||||             | |||
297 TTCTCTTCTTGGCTTGGCTTGACTAAATTGGT.............TGTGC 333

579 AGGGCAAGGTGGCGCTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTC 628
    | |||||||||||||||| |||||:|||| |:| ||||||| |||||| |
334 ACGGCAAGGTGGCGCTGATGTCNNCGGGAANCATGCACCAACTGCACATA 383

629 TTCATCTTCGTGCTCGCGGTCTTCCATGTCACCTACAGCGTCATCACCAT 678
    |||||||||||||||||| |||||||| |||   |||||||| |||||||
384 TTCATCTTCGTGCTCGCCGTCTTCCACGTCTTGTACAGCGTCGTCACCAT 433

679 AGCTCTAAGCCGTCTCAAAGTGAGCCTTTGCTTCTTCTTCTTCTTCTTTT 728
      | |||||||||||||||||||||| |      ||
434 GACCCTAAGCCGTCTCAAAGTGAGCATCATACTC..............  467

729 ACCGCACGTCTGTCTGTCAGGCGTACCTACCTGTTCATCAGGCTTGAGTA 778
          |||| |||||     | | |     |||     |   |      |
468 ......GAGCTGTTTGTCAATAATCCTT...GGTTTCCAATCCAATTCCA 508

779 AAACTGTTCCATAATCTGCTCCGGCATAATCCTCTCCTCCTGCAGATGAG 828
    || |||    |   |  |||||||||             | ||||||||||||
509 AAGCTGGCACTGATCCTGCTCCGG.....CTTCCTGCAGATGAA 547

829 AACATGGAAGAAATGGGAGACAGAGACCACCTCCTTGGAATACCAGTTCG 878
     |||||||||| |||||| | |||||| |||| |||| || ||||||||
548 GCAATGGAAGAAGTGGGAGTCGGAGACCGCCTCGCTGGAGTATCAGTTCG 597

879 CAAATGGTCAGGATCCCCCACTCTGCAATCTCCCCTTCTTCGAAACCAAA 928
    | |||||||||                 || |   | |||  |   |||
598 CGAATGGTCAG.................CTTCAACTTTTCTTACTGAAA 629

929 CCTGATGATCCATTT...AAAGACGCAGGCACGATCA.....GAGTGAGT 970
    || ||||   |||||   | | ||||| |||||||||       |  | ||
630 CCGGATG...CATTTACAACAAACGCACGCACGATCAATCATCACAGTGT 676

971 GAACTGAT.GTATGTTCATTTTTTGTGTCCT.TTCAGATCC..TGCACGG 1016
    || | |||    ||  |    ||    ||||   |||||||  |   |||
677 GAGCCGATACGTTGAACCCGATTGAAATCCTCCGCAGATCCCATCGCCGG 726
```

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FIGURE 6 c nt'd

```
1017 TTCCGGTTCACGCACCAGACGTCGTT.CGTGAAGCGCCACCTGGGCCTCT 1065
      | ||||||||||||||||||||| ||||  |||| ||| ||||||||||||
 727 TGCCGGTTCACGCACCAGACGACGTTGGGTGAGGCGGCACCTGGGCCTCT 776

1066 CCAGCACCCCTGGCATCAGATGGGTGGTGAGTTTTTTAGCTTCTTATCTG 1115
      |||||||||| ||| ||||||||||
 777 CCAGCACCCCCGGCGTCAGATGGGT..........................  801

1166 GCCTGTGATGTTTGTTGCCTTGTCAGGTGGCCTTCTTCAGGCAGTTCTTC 1215
                                ||||||||||||||||||||||||
 802 ........................GGTGGCCTTCTTCAGGCAGTTCTTC 826

1216 AGGTCAGTCACCAAGGTGGACTACCTGACCTTGAGGGCAGGCTTCATCAA 1265
      | ||| || ||||||||||||||||||||||| ||   ||||||||||
 827 ACGTCGGTGACCAAGGTGGACTACCTGACCTTGCGGCAGGGCTTCATCAA 876

1266 CGTACGTGCCTCCCCTTCTAGCTCCGCCATTGCTGCCGCGATGTAGCAGC 1315
      |
 877 C..........................................  877

1366 CAAATTATTCTGCGCAGGCGCATTTGTCGCAAAACAGCAAGTTCGACTTC 1415
                      |||||| | |||||   || || ||||||||||
 878 ..................GCGCATCTCTCGCAGGGCAACAGGTTCGACTTC 910

1416 CACAAGTACATCAAGAGGTCGATGGAGGACGACTTCAAGGTCGTCGTCGG 1465
      |||||||||||||||||||| |||||||||||||| ||||||||| |
 911 CACAAGTACATCAAGAGGTCGTTGGAGGACGACTTCAAAGTCGTCGTCCG 960

1466 CATCAGGTACGTTCCATTCCTTCCTCTGCAC.....CACACCACAC 1506
      |||||||||||  |||||||| ||||||||      ||  |  |||
 961 CATCAGGTACGCGCCATTCCTTTCTCTGCACAAATTAATACATCCACCAC 1010

1507 CCCATGGATAGATTTTAACAATTGCTGTCAGGTTCCACATGATAACAATA 1556
      | ||| : |||||    | |                 ||  :  |:| ||
1011 CACATANGTAGATAGATAGA.............TCGATANATANATTA 1045

1557 TACTATGAACTTGGTCTTTGCTCCTTGTCCTTGCACGATCATGACACATT 1606
      ||| | |  |  |  | |   | | | || |   | |||| ||||||||
1046 TAC.AAGTGCCGGTACGTACGTACGTCTCAT...ATGATCTTGACACATC 1091

1607 TGGCCTGTTTTCGCAGCCTCCCGCTGTGGGGTGTGGCGATCCTCACCCTC 1656
      || ||| ||  |||| ||| ||| ||| |||   |||||| |||||| ||||
1092 TGTCCTCTTGCCGCAATCTCAAGCTCTGGTTCGTGGCGGTCCTCATCCTC 1141

1657 TTCCTTGACATCAATGGTATGGACCTTCTCC.TCTCCGGTTTCTCTATTG 1705
      |||||||| || | ||||  |||| ||| |  || | |   |  |
1142 TTCCTTGATTTCGACGGTAGCCGCCTTGTCCATGCCCTGCTCGCCCTCTC 1191

1706 CTTTGCAGCTAAATAAAACACTTGCAATTCGTCTCGTGATCACCGCTCAT 1755
      ||  ||  ||    | ||    || || | ||| |||           ||
1192 CTCCGCTTCTCTCCATAATTTGTG.AACTTGTCCCGT.........AT 1229

1756 TTTTCAACCATTTCTTTTTCTACTCATAGGGG.TTGGCACGCTCATCTGG 1804
      |  | ||     | |  ||| |||  ||||| | ||||| ||  ||||||
1230 ATAACCACACCACCGTCGTCTTCTCGCAGGGGATCGGCACTCTTCTCTGG 1279

1805 ATTTCTTTCATCCCTCTCGTGGTAAGTGCAGATTTCTCCATCGAAAGCAA 1854
      || ||  |  | |||||||||||||||| ||       | ||   ||   |
1280 ATGTCCGTGGTTCCTCTCGTGGTAAGTCCA.......CAATTTGAATAGA 1322

1855 CAGCAAACCCAATTTGATCGCAATGGAAACCCACACCTAATATTAACTCA 1904
      || |    ||||||     | |  | |   ||| || |||       | |
1323 CAACCTGTCCAATTGTGATGTACAGTACCTCCAAACTTAA.......TTA 1365
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1905 AAATGTCAATTGTCGGTGCGTCTTCC.....TCAACAGATCCTCTTGTGT 1949
     | ||||||  |||  | |  |||||  |       ||  ||||||||||||||
1366 ACATGTCATTTGCTGAT..GTCTTGCGTGTAACATTAGATCCTCTTGTGG 1413

1950 GTTGGAACCAAGCTGGAGATGATCATCATGGAGATGGCCCTGGAGATCCA 1999
     |||||  |||||||||||||||| | ||||||||||||||||  |||:|||||
1414 GTTGGGACCAAGCTGGAGATGGTGATCATGGAGATGGCCCAGGANATCCA 1463

2000 GGACCGGGCGAGCGTCATCAAGGGGGCCCCCGTGGTCGAGCCCAGCAACA 2049
      |||||||  |||||||  |||||||  ||  ||||  ||||||||||||||||
1464 TGACCGGGAGAGCGTCGTCAAGGGTGCTCCCGCCGTCGAGCCCAGCAACA 1513

2050 AGTTCTTCTGGTTCCACCGCCCCGACTGGGTCCTCTTCTTCATACACCTG 2099
     |||  ||||||||||  ||||  ||  ||||||||||||||  ||||  |||||
1514 AGTACTTCTGGTTCAACCGGCCTGACTGGGTCCTCTTCCTCATGCACCTC 1563

2100 ACGTTGTTCCAGAACGCGTTTCAGATGGCGCATTTTGTGTGGACAGTGGT 2149
     ||   | ||||||||||||||||||||||||  |||||  ||||||||||||||
1564 ACACTCTTCCAGAACGCGTTTCAGATGGCTCATTTCGTGTGGACAGTGGT 1613

2150 ACGCCACCGATGAACTTGTCAGTTAACATGGG..................  2181
     |    |:    | | ||||||||  ||  ||  | :|
1614 A...CNTACAAGTACTTGTCACTTCACTTANGCTAACTCCAACAAACGAA 1660

2182 .........TGTCAAGGCACCGAGTGCCGCTGATGAACTGCTCTGACGGAG 2223
                |||||  ||  ||  | |       |   |  | | |  ||  |
1711 GACACAAAACTCAATCCAACGCGCGGTAGCAAACGAACGTTTTTCCGTAC 1760

2224 ATTTAC.....................................TTG 2232
      |||  |                                    |||
1761 GTTTTCGTCCGCTTTCGCCCCATCCCAGCCCAAATTCGTTGACGTTGTTG 1810

2233 TGTTGTAGGCCACGCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGG 2282
       |  | |||||||||||||||||||||||||||||||||||  |  |  ||  |
1811 CATCGCAGGCCACGCCCGGCTTGAAGAAATGCTACCACGAGAAAATGGCA 1860

2283 CTGAGCATCATGAAGGTGGTGGTGGGGCTAGCTCTCCAGTTCCTCTGCAG 2332
      ||||||||    |||||  |||  |||||  ||||   ||||  ||  |  |||||
1861 ATGAGCATCGCCAAGGTCGTGCTGGGGGTAGCCGCCCAGATCTTGTGCAG 1910

2333 CTATATGACCTTCCCCCTCTACGCGCTCGTCACACAGGTAATAAAACCGT 2382
     :||  ||  ||||||||  ||:|||||||||||||
1911 NTACATCACCTTCCCGCTNTACGCGCTCGTCAC.................  1943

2433 AATCATCTGTGTGTGCTGGCTTTGTATGCAGATGGGATCAAACATGAAGA 2482
                                      |||||||||  |||  |||||||||
1944 ..........................GCAGATGGGCTCACACATGAAGA 1966

2483 GGTCCATCTTCGACGAGCAGACGTCCAAGGC.GCTCACCAACTGGCGGAA 2531
     |    ||:|||||||||||||||||  |||||||  |||  ||||||||||||  ||
1967 GAAGCANCTTCGACGAGCAGACGGCCAAGGCGGCTGACCAACTGGCGAAA 2016

2532 CACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATGCTGATGGCTC 2581
      | ||||||||||||||||||  |  |||||||  |||  ||||||||||||  |
2017 GATGGCCAAGGAGAAGAAGAAGGCCCGAGACGCGGCCATGCTGATGGCGC 2066

2582 AGATGATCGGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATGCCGAGC 2631
     |||||   |||||  |||  ||  ||||||    ||||:|||||||
2067 AGATGGGCGGCGGCGCGACGCCGAGCGTCGGCTNGTCGCCG.........  2107
```

FIGURE 6 cont'd

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2632 CGGGGCTCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGA 2681
                  |||||||||||| |||||||  |   ||  ||||||  ||
2108 ...............GTGCACCTGCTCCACAAGGCCGGGGCGCGGTCCGA 2142

2682 CGACCCCCAGAGCGCGCCCACCTCGCCAAGGACCCAGCAGGAGGCTAGGG 2731
     |||||||||||||||  |||   |  ||  ||  |||  ||  ||  ||||  |    |  |
2143 CGACCCCCAGAGCGTGCCGGCGTCCCCGAGGGCCGAGAAGGAAGGCGGCG 2192

2732 ACATGTACCCGGTTGTGGTGGCGCACCCGGTGCACAGACTAAATCCTAAC 2781
      |                 |||   |||  ||||  ||  ||    ||   ||||
2193 GC...............GTGCAGCATCCGGCGCGCAAGGTACCTCCTTGT 2227

2782 GACAGGAGGAGGTCCGCCTCGTCGTCGGCCCTCGAAGCCGACATCCCCAG 2831
     |||  ||  |||||||  |||||||||  ||||  |||||  ||   |||||||| |
2228 GACGGGTGGAGGTCGGCCTCGTCGCCGGCGCTCGACGCTCACATCCCCGG 2277

2832 TGCAGATTTTTCCTTCAGC..........CAGGGATGAGACAAGTTTCTG 2871
     ||||||||||  |||||||           |  |||  |||||||||  ||
2278 TGCAGATTTTGGCTTCAGCACGCAACGTTGACCGATCAGACAAGTTCCTT 2327

2872 TATT 2875
     |  ||
2328 TTTT 2331
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Figure 7


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                                                                  GGCTGCTCCGCCAGCAAACCAGACACACAGCAGCGTACCTGCGT
                                                                  ACGTAGCGTCGCGTTTCTTTTTTTTCCTTTCGCCTCTCTTGCTTGCTCCGGCCGGCCACG
                                                                  TCGATAGCCGGCCACGGCCAGGCACCTCGCGGTTGCGTCGCGTGCATCTGCGTGTGCGTA
                                                                  CCTGGTAGAGGCGGCCGTCTGCTTGCTCCGGGCAAGGAAGCAGGTTGCGGCGGTCGACCG
                                                                  M  S  D  K  K  G  V  P  A  R  E  L  P  E  T  P  S  W  A  A  V      20
                                                                  ATGTCGGACAAAAAAGGGGTGCCGGCGCGGGAGCTGCCGGAGACGCCGTCGTGGGCGGTG      60
helix I                                                           A  V  V  F  A  A  M  V  L  V  S  V  L  M  E  H  G  L  H  K      40
                                                                  GCGGTGGTCTTCGCCGCCATGGTGCTCGTGTCCGTCCTCATGGAACACGGCCTCCACAAG     120
                                                                  L  G  H  W  F  Q  H  R  H  K  K  A  L  W  E  A  L  E  K  M      60
                                                                  CTCGGCCATTGGTTCCAGCACCGGCACAAGAAGGCCCTGTGGGAGGCGCTGGAGAAGATG     180
                                                                  K  A  E  L  M  L  V  G  F  I  S  L  L  L  I  V  T  Y  Q  H  R      80
helix II                                                          AAGGCGGAGCTCATGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGACCCC     240
                                                                  I  H  I  A  K  H  I  C  I  S  E  D  A  A  D  V  M  W  P  C  K  R     100
                                                                  ATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTCATGTGGCCCTGCAAGCGC     300
                                                                  G  T  E  G  R  K  P  S  K  Y  V  D  Y  C  P  E  G  K  V  A     120
                                                                  GGCACCGAGGGCCGCAAGCCCAGCAAGTACGTTGACTACTGCCCGGAGGGCAAGGTGGCG     360
                                                                  L  M  S  T  G  S  L  H  Q  L  H  V  F  I  F  V  L  A  V  F     140
helix III                                                         CTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTCTTCATCTTCGTGCTCGCGGTCTTC     420
                                                                  H  V  T  Y  S  V  I  T  I  A  L  S  R  L  K  M  R  T  W  K     160
                                                                  CATGTCACCTACAGCGTCATCACCATAGCTCTAAGCCGTCTCAAAATGAGAACATGGAAG     480
                                                                  K  W  E  T  E  T  T  S  L  E  Y  Q  F  A  N  D  P  A  R  F     180
                                                                  AAATGGGAGACAGAGACCACCTCCTTGGAATACCAGTTCGCAAATGATCCTGCACGGTTC     540
                                                                  R  F  T  H  Q  T  S  F  V  K  R  H  L  G  L  S  S  T  P  G     200
                                                                  CGGTTCACGCACCAGACGTCGTTCGTGAAGCGCCACCTGGGCCTCTCCAGCACCCCTGGC     600
                                                                  I  R  W  V  V  A  F  F  R  Q  F  F  R  S  V  T  K  V  D  Y     220
                                                                  ATCAGATGGGTGGTGGCCTTCTTCAGGCAGTTCTTCAGGTCAGTCACCAAGGTGGACTAC     660
                                                                  L  T  L  R  A  G  F  I  N  A  H  L  S  Q  N  S  K  F  D  F     240
                                                                  CTGACCTTGAGGGCAGGCTTCATCAACGCGCATTTGTCGCAAAACAGCAAGTTCGACTTC     720
                                                                  H  K  Y  I  K  R  S  M  E  D  D  F  K  V  V  V  G  I  S  L     260
helix IV                                                          CACAAGTACATCAAGAGGTCGATGGAGGACGACTTCAAGGTCGTCGTCGGCATCAGCCTC     780
                                                                  P  L  W  G  V  A  I  L  T  L  F  L  D  I  N  G  V  G  T  L     280
helix V                                                           CCGCTGTGGGGTGTGGCGATCCTCACCCTCTTCCTTGACATCAATGGGGTTGGCACGCTC     840
                                                                  I  W  I  S  F  I  P  L  V  I  L  L  C  V  G  T  K  L  E  M     300
                                                                  ATCTGGATTTCTTTCATCCCTCTCGTGATCCTCTTGTGTGTTGGAACCAAGCTGGAGATG     900
                                                                  I  I  M  E  M  A  L  E  I  Q  D  R  A  S  V  I  K  G  A  P     320
                                                                  ATCATCATGGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCGTCATCAAGGGGGCCCCC     960
                                                                  V  V  E  P  S  N  K  F  F  W  F  H  R  P  D  W  V  L  F  F     340
                                                                  GTGGTCGAGCCCAGCAACAAGTTCTTCTGGTTCCACCGCCCCGACTGGGTCCTCTTCTTC    1020
                                                                  I  H  L  T  L  F  Q  N  A  F  Q  M  A  H  F  V  W  T  V  A     360
                                                                  ATACACCTGACGTTGTTCCAGAACGCGTTTCAGATGGCGCATTTTGTGTGGACAGTGGCC    1080
                                                                  T  P  G  L  K  K  C  Y  H  T  Q  I  G  L  S  I  M  K  V  V     380
                                                                  ACGCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGGCTGAGCATCATGAAGGTGGTG    1140
helix VI                                                          V  G  L  A  D  Q  F  L  C  S  Y  M  T  F  P  L  Y  A  L  V     400
                                                                  GTGGGGCTAGCTCTCCAGTTCCTCTGCAGCTATATGACCTTCCCCCTCTACGCGCTCGTC    1200
                                                                  T  Q  M  G  S  N  M  K  R  S  I  F  D  E  Q  T  S  K  A  L     420
                                                                  ACACAGATGGGATCAAACATGAAGAGGTCCATCTTCGACGAGCAGACGTCCAAGGCGCTC    1260
                                                                  T  N  W  R  N  T  A  K  E  K  K  K  V  R  D  T  D  M  L  M     440
                                                                  ACCAACTGGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATGCTGATG    1320
                                                                  A  Q  M  I  G  D  A  T  P  S  R  G  S  S  P  M  P  S  R  G     460
                                                                  GCTCAGATGATCGGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATGCCGAGCCGGGGC    1380
                                                                  S  S  P  V  H  L  L  H  K  G  M  G  R  S  D  D  P  Q  S  A     480
                                                                  TCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGACCCCCAGAGCGCG    1440
                                                                  P  T  S  P  R  T  Q  Q  E  A  R  D  M  Y  P  V  V  V  A  H     500
                                                                  CCCACCTCGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGGTTGTGGTGGCGCAC    1500
                                                                  P  V  H  R  L  N  P  N  D  R  R  R  S  A  S  S  S  A  L  E     520
                                                                  CCGGTGCACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTCGTCGTCGGCCCTCGAA    1560
                                                                  A  D  I  P  S  A  D  F  S  F  S  Q  G  *
                                                                  GCCGACATCCCCAGTGCAGATTTTTCCTTCAGCCAGGGATGAGACAAGTTTCTGTATTCA
                                                                  TGTTAGTCCCAATGTATAGCCAACATAGGATGTGATGATTCGTACAATAAGAAATACAAT
                                                                  TTTTTACTGAGTC
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Figure 8

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   1  GAATTCAATT AAGGACAACA ACGGATGATA GGCTTAAGCT AGAGAGGATT
  51  CATATGGATT AATTAACTGT ACTTAAGTTG AGGTAAAACT CTATCGATTG
 101  CTTTGGACAC CGGCTCTCCC ATGATCTGCC AAGTTGAGCC GGCCTACCTA
 151  ATTTTCTTCG AAAGCACACA ACAAACGAAG GTAACCACTA ATCTAGACAC
 201  CACGCCTAAG TTATCAATTA CTACTCTAGT CTCGCGTAGA AACTTCATTC
 251  TTTATGGAGA GTGCTAGTAC TAGAGTACTT AATATAATAG TAAGCGACAA
 301  ACCCACGACG ATGAGAATGT ACCTCACTTA CGTAGTCAAT TAAGTCGAAA
 351  AGGAAATCTT GAACACTTAC TTTATTAAAG AAGTATTCCC CGAGGTACAG
 401  GAGAGGAGAG CACGCCAATA ACTCCAGCAC TCCTCCGAAA CCTTTCTCAC
 451  TCTCTACCCT TTTTCTCCAC ACAACTAAAA TGATGTCTAA TGTATGAAAG
 501  TGAGTTGTAC TCTATTTTGT TGTGTGTTTG GAAGTGAAAT TAGCTCATCC
 551  TTTTATAGCA ACTTAATGGT CGGTTGTAGG TTGGTAATTA AGTCGGTAAA
 601  CACTCACAAC CACCATCGTC AACCAATAGG AGATCGCCAC ATGATCGAAA
 651  GCTGACAGTT AGGGGTGCCA ACCCTGTTTT GTCCGAACCA AGCAAACAAC
 701  CTCTATCTAG GACCTCTCTT CTATGTCTGA CAAGTCGGCC CATATGGCGG
 751  TGCACTATGG ATTAAGTCAA TTTCAGTCGT TTTGGACTGT CATGTGGGCC
 801  CTTCCAATCC TTGTGCTCCC ATATGATTGG TCGAAAGTAC ATTTAATTCC
 851  TGGGTGAGTG CTAGAACTAA TATGATAGAT GTGCTCCGGC TCCTGGGAAA
 901  GAGGCCACTT GACATACTTG GGGTAGTGCC CCAAGGGTAT TCCCTATCGC
 951  TTTTTCATAA TTTTCTCTCT CCAAAATCGG ACGGAAACAA TAAAAAAGAG
1001  AGGCGATGTT CATCGGCAAA TATCTATTTT TTTGATAGTG TCTTCCCTTA
1051  AAACTTGATT TTTGCGAAGA CTTCCGGCTA AAACCATGAA ATCAGAGTTC
1101  CTTGTAACAA ATTTAATTTG CCTAAATACA AAAAAGATCG AATGGAGATA
1151  GCATTAAACT TGCTCCATAC GAATCATATT AGTTGGACCG TAACTCATAG
1201  AAAAAGTTGC AAGTTGGTTG ACCTATCAAC CCTCTTATGT TGACCGTAAA
1251  CCTGTTATGC ATTAAGGATT AAGTACCGGC AGATCGTCAC TACTCACGAA
1301  TGCACAAATT TCCGGTAACG TAGGATGGGA TGAGTTGGTC ACAAACGGGT
1351  CACCACGTCG CCCAACCTGC CGCGATCGAG CCATTGGCCG GCGATGCACG
1401  CGCTTTGACA CAGCCGCCCG CCGCCCCCCG GCCCGCCCCC GTTTTTAATA
1451  AAAACCGGCC GCCCCCTGTC AAAGGTGTCA AAGTGTCAAG TGCATCAGAG
1501  CTAAGCTAGC GGTCACCCAG TCAGCTCACC CCGAGACGCA CCAGGGGATC
1551  TATCGGATCA TGGCAGGTGG GAGATCGGGA TCGCGGGAGT TGCCGGAGAC
1601  GCCGACGTGG GCGGTGGCCG TCGTCTGCGC CGTCCTCGTG CTCGTCTCCG
1651  CCGCCATGGA GCACGGCCTC CACAACCTCA GCCATGTACG CGCGCGCGCA
1701  CGCGGTGTGC TCATCTCTCG AGTTAATTTG GTTGTTGTTG TTGTTGTGTT
1751  CTTGTGACAT CTCAATTAAC ATCCGATCGT GGTCGATCGA TCGCCCTGTG
1801  GTGGCGATAC TGCTTGCATT GCAGTGGTTC CGTAGCCGGC AGAAGAAGGC
1851  CATGGGCGAC GCCCTCGACA AGATCAAAGC AGGTCACCCT CAGCCTCAGC
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FIGURE 8 cont'd

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1901  TCACCCTCAG CCTCCATCTC TAAATATTTG ACGCCGTTGA CTTTTTTAAA
1951  TATGTTTGAC CATTCGTCTT ATTTAAAAAA TTTAAGTAAT TATTAATTCT
2001  TTTTCTACCA TTTGATTCAT TGCTAAATAT ACTATTATGT ATACATATAG
2051  TTTTACATAT TTCACTAAAG TTTTTAAATA AGACGAATGG TCAAACATGT
2101  TTAAAAAAGT CAACGGCGTC AAACATTTAG GAAGAAGAGA ATATTATATT
2151  GCTGCTCCCC TCTAGCCACT TTGCTGCCTC CCTCGTCATT TTTTCAAGTA
2201  TTTTACGCAA GACTGGTCCT CCAAATCAAA CGTCACAAAT AAGCCATTTA
2251  TAGTTTCCTT TCGCTTTTTA AGGGGGACTA CTTGTATTTA ATCATGGAGG
2301  AAACTACCAG TCGGATGTCC GATTACTTAA AAAAAATTC GGGGGACTAA
2351  TTTTTTTGGC TGATCATCGG TGAAATATTA GGTTATATAT GTTGAAAAAA
2401  AATCAGCCAC AAACAATGAA ATATTTTGTG AAACACATAT TAGACACGTT
2451  GAAACGTATC ATTGTTACGT ATAAAACATC GAATGTTAAC AGATTAAAAC
2501  ATATGTTTTT TTTTAATCAG AATATAATCA TGCGATATAT TATTGTAAAG
2551  ATATAATTAC AACGAATACA ACAGTGCGAT CGGATTATAT ATATATTAGT
2601  AGTTTAAGAG AAAAATCATT TTGAAGATTA CTAGATACAT ACACGTATAG
2651  ATGGATGAAG TGGAGAGAGA TTAGAGATAA GTAGTTATAT GAATTTTGTG
2701  AAACACACTT AAGACATATG TTCAAACATA CTGCTATTAT GTATGAAATA
2751  TTGAGTTTTA ACGGTTTAAA ACACATATTC TTTTAATTAG AATGTAATAA
2801  TGTGATATCT TGTTGTAAAA TTTAATTACA TCTAATATAA CGGTGTGATT
2851  AGATTGTATG TTGGATAACA TGCCCATCGG TTGGCTTATT TAGGGAATAA
2901  GCCAAATGGT ATATTTGCAA ACGAAAAATA ATTTGTAAAT AAAACTTTTA
2951  TGTATGTATT CTTAACGATC TAGCAGCAAA GGCTGAAAAA TAAACTTCGA
3001  TGAAAAATCT CAAAATCAAC TCTTAAAATT TAAATTTTGG CTTATAAGTA
3051  TAGTTCCTAA CTAGTTTAGA AGAAAAAATA TTTAAAGCGG GGAAGAGGAA
3101  AAGGAATAAA CTAATAGCTA AATTATTGCA TGCATGTAGC GATTTGAGGA
3151  CGACCGAGTT GTTTTGTCTG GATCAGCCGA CCGAGACAGA GCAATCTTCT
3201  TTAATCATAA ATAACCAGAA AAACCATACC AGTTCATCAC AATGGACCGA
3251  GTCAGAGTCA TTACATATTT TTCATTGTTG CGCACAGGAT TCACCATGTT
3301  CTTATGGGAA ATATTTTTAA CTCTCAAATG GTTATGATTT TGAACTCTCA
3351  TTTTTGAGAG AGAATTAACA AGCGAGCGAG CAATCAGGCC AAAAAGGGAG
3401  AAAGAAAATT ATTTTTGTTA ATTTTTTTTT AAGGTAGGGT GGAGGAGTCA
3451  TTACATGATT TTTTTTTATA TTCCCTCGTT GATTATATGC TGTTCAAATG
3501  GTTATGATTT TTTTAAAAGA TAACAACAAT ACAAATTAGT ATGTGATAGA
3551  TCATTTCACG AGCATATAGG ATTAAATTTA ACTTCTGTAA ATTACAAAAC
3601  AAACAAGTTT AACTGTTAAT ATACATTAAA TTTGTTTTTT TCAACTTAGG
3651  AATTGAATTT TATGTATATA TTTGTAAAAT GATATATTAA TTTATTTTTT
3701  TAAAAAAATA ATTATTTAGA TAACACGCAA ACTAGAAAAC CACCGCAGAA
3751  GTTCTCATAT TTCTTGTCCT ATCTGCACTT GCAGAGCTGA TGCTGCTGGG
3801  CTTCATATCC CTGCTTCTCA CCGTGGCACA GGCGCCCATC TCCAAGATCT
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FIGURE 8 cont'd

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3851  GCATCCCCAA GTCGGCTGCC AACATCTTGT TGCCGTGCAA GGCAGGCCAA
3901  GATGCCATCG AAGAAAGAAG CAGCAAGTGG TCGCCGGTCC TTGGCCGGCG
3951  CCGGCGGCGG GGACTACTGC TCGAAATTCG ATGTGAGAAT AACACCAGCT
4001  GCCGGCAAGC ACAACCTCGA TGCAATAACT AATTTAACTA TAATTGATTT
4051  TTCTTGGGTT TTCTGCAGGG CAAGGTGGCG CTGATGTCGG CAAAGAGCAT
4101  GCACCAGCTG CACATTTTCA TCTTCGTGCT CGCCGTGTTC CATGTTACCT
4151  ACTGCATCAT CACCATGGGT TTAGGGCGCC TCAAAGTGAG TTTGTCGTTC
4201  TGTCCCTCAT GCACATGTTT TCTCTAGTTC TAGCAAGATT GTCAGTCCTT
4251  CAAATGGATT GTTTCGACAA GAAACCCAAT TTATTAATTT GCCAGTAAAT
4301  ATATAATAAT TGATCTTTCT TGGTTTTAGA TGAAGAAATG GAAGAAGTGG
4351  GAGTCACAGA CCAACTCATT GGAGTATCAG TTCGCAATCG GTAGTGAATT
4401  AAGAATCTCC CTAACTATTT CATTTCAGAA CCTTTATGAT AATGTCTTGA
4451  AAGAGGAGGA GCAAATCAGC TGAAAAATAT GATCGATCCA TGCAGATCCT
4501  TCACGATTCA GGTTCACGCA TCAGACGTCG TTCGTGAAGC GGCATCTGGG
4551  ATCATTCTCA AGCACCCCTG GGCTCAGATG GATCGTGAGT TATCAATCTC
4601  CGAATACATG CTTGTTTTTT ATTCTTGCAA CTGGCCTAGC TGTTCCAATT
4651  CAATCCATAT TTTTTGAAAA AAAAAATATT CATGCCGTGT TTGTTGTTAG
4701  GTAGCATTCT TCAGGCAGTT CTTTGGGTCC GTCACCAAGG TGGACTACCT
4751  GACCATGCGG CAAGGCTTCA TCAATGTATA TACTAATCAA ACCTGACCAA
4801  TTCAACATTG ATGATGCAAA CAGAGACCAG GTTTTTTTTT TCGAGTGTGC
4851  ATTGAGTAAT GGTTTTAGCT TCTTCTCTTT TGCAGGCGCA TTTGTCGCAG
4901  AATAGCAAGT TCGACTTCCA CAAATACATC AAGAGGTCTT TGGAGGACGA
4951  CTTCAAAGTT GTCGTTGGCA TCAGGTCCGT CCTCGCTTTA TTAATTATAG
5001  GACTCTTATA TTCAACATTT TTTTTATAAA GAAACATATT TAGTCTCCAG
5051  TTGTGTATGT GTATGTGGAT CTTGACACAT TTGGCTGGTT TTGCAGCCTC
5101  CCTCTGTGGT TCGTCGGAAT CCTTGTACTC TTCCTCGATA TCCACGGTAA
5151  TCCTTGTCCT ATTTCATTCT TTTTTTTACT CTCAAAACCT TGTTCTGAAT
5201  TGGTCTTATA ATCACCATCG ATTTTTTTTC AACTTTTTCC CCGCGTGTAG
5251  GTCTTGGCAC ACTTATTTGG ATCTCTTTTG TTCCTCTCAT CGTAAGAGCG
5301  AAATTTCCCT GTCCAAAGAA ACAGTTAACA TAATTAATTA TGCTTTAATT
5351  TATCATGAAA ATTAATATGA TCATATAACT AATGAACAAA CATTCATGTG
5401  AATGCCACCG TTGTCTCAGA TCGTCTTGTT AGTTGGGACC AAGCTAGAGA
5451  TGGTGATCAT GGAGATGGCC CAAGAGATAC AGGACAGGGC CACTGTGATC
5501  CAGGGAGCAC CTATGGTTGA ACCAAGCAAC AAGTACTTCT GGTTCAACCG
5551  CCCTGACTGG GTCTTGTTCT TCATACACCT GACACTCTTC CATGTACATG
5601  TTTAAAACCT AAACCTTGCT GCTCAACTAC AAATAGTACT TTATCTTTCA
5651  CAATTAACAC CTAATTAACT AACATAGCAT CCATCCATTT GTGGCTACTG
5701  ATCGATGGGA CGACGGATCG ATCATCACCA GAACGCATTT CAGATGGCGC
5751  ATTTCGTATG GACTATGGTG TGTATGCTAC TTGCTTAGTT GTTGCCATTA
```

SUBSTITUTE SHEET (RULE 26)

Figure 8 cont'd

```
5801  TCAGTTCTTA AGCAAATTAA GTGTGATGCA TGCACTGACT AATGAGACAA
5851  AAAATGACAC AGCTTGTTCA TCGATCTGGT TGTTTTGTGT GTGACAGGCA
5901  ACACCTGGTC TGAAGAAATG CTTCCATGAA AATATTTGGC TGAGCATCGT
5951  GGAAGTCATT GTGGGGATCT CTCTTCAGGT GCTATGCAGC TACATCACCT
6001  TCCCGCTCTA CGCGCTCGTC ACACAGGTGA ACAAGCCATT CACAAATTCT
6051  ATTAGCCGTT TCTTAATTGA TGACACTGTT AATTTTTAGA CACACGTTTT
6101  GACCATTTGT CTTATTAAAA ATATTTATGT AATTATCATT TGAGTTGTTT
6151  TATCACTAAA AGTACTTTTT AAATAATTTA TATTTTGCAT TTGTACAATT
6201  CTTTTAATAA GATAATGGTC AAACATGTGT CCAAAAGTTA ACAGCATCAT
6251  CTATTAAGAA AAGGAGGGGT TTTTTTTTTT TGGAATTTTG CAAAATTTGT
6301  TCAAAATCAG TCCAAAACCT TTTTTTTTTT CGAAATTTCA GTTTCACTAC
6351  CAGTCCCCAT AAAATGTCTT TTCTTTATTT CCACAAGATT GAACCCATGA
6401  GATGCCCTTT GTGTTGGTAT GTGTTTTGGC CATCACTTGC AGATGGGATC
6451  GAACATGAAG AAGACAATTT TCGAGGAGCA AACGATGAAG GCGCTGATGA
6501  ACTGGAGGAA GAAGGCGATG GAGAAGAAGA AGGTCCGGGA CGCCGACGCG
6551  TTCCTGGCGC AGATGAGCGT CGACTTCGCG ACGCCGGCGT CGAGCCGGTC
6601  CGCGTCGCCG GTGCACCTGC TGCAGGTCAC AGGGCGGGTC GGACGCCCGC
6651  CGAGCCCAAT CACGCTGGCC TCACCACCGG CACCGGAGGG GACATGTACC
6701  CGGTGCCGGC GGCGGCTGCG TCTCGCCAGC TGCTAGACGA CCCGCCGGAC
6751  AGGAGGTGGA TGGCATCCTC GTCGGCCGAC ATCGCCGATT CTGATTTTTC
6801  CTTCAGCGCA CAACGCTGAC GGGGGCGATC GGTTTCTGTA TTGATGCTGT
6851  ACCAAACATA GGAGTTTAAT ATATATATAA TTGTTACGGT AAAATCTAAT
6901  TATTGTGCGC GCACTTATAT TAGTCTTATA GCGCGACTGG TTCGTGATTA
6951  GACAAGGTGA TGCATGCTGT TTAGTTATAA AGGATATCAG CGCAGCTAAA
7001  AAAACTTACT CCCTACTTAA TAGATGACCT CGTTGATTTT TAACATTATT
7051  CGTCTTATTT AAAAAATTTA TGCAAATGTT TAAAACATAA ATCATGCTTA
7101  AAGTACTTTT AGTGATAAAA CAACTTACAA CAAAATAAAT TATAGTTACC
7151  TAATTTTTTT TAATAAATCG AATGG
```

SUBSTITUTE SHEET (RULE 26)

```
1     TTATACCATG TGAGAAAGGC TGGAAGCATA TGCTCTTAGC AGGGACGCGT
51    GCATGTTTAT ATAGGAGGCA TAAGCCGAAG AGATATACAT GAGGAGAGGT
101   TTAAGATCAG TCTATCTTAT TTACAGTTTA AACACAAGGA GATAGAAAGA
151   GATCCTAACC TACACATGTT ATACAAGTCA CGTATAATAC AAGAGTTATT
201   TCGTCTAACA CCCTCCCCTC TGATATGATA AGTCGCCGGG AGAGAGAGAG
251   AGTGTGTGGC TGCCCTCGCT GCACTGCACG CACATGTTTA CTTCTCCGAC
301   TGAAACCACG GTGAAACCGG CGGCGGTGTC GCACTCCCCT GACTTTCCTC
351   GCCGGGGTCC CGTCCGGACA ATTAAACCGT CTGTACCTGC CGGGCGTCGA
401   CCCGATCGTG ATGTGGCGCC GCTTTGTCTG CAGCGAGCTG CGTGGCCGAT
451   GGCAACAAAA CTGCGGTCAC ATACATGCAT ACCCCGCATA CCCCGACGCT
501   CACCAGTAAG TAGGCTGTGG TGCGGCACCA CGGGCTCGCC GCCATTCATG
551   CCATGCATGG GCCACCCGCC GGCGAAACCG CGGCGCTGCT GCCTGCCACC
601   CCGCCGCCGT TGACGAAGAC TTCGCCCGGC CATCCATAAA AGCATGCATG
651   GCTTGCTCTC ACCGGTCCGG CCACACACAC CACACTTCAC TTCGCCATTC
701   GCACCACCGA GAGCGTAGCG TAACGTGTGT TTGAAGTCCT ACCATTAATT
751   TTGCTGGATC GATGGCTGGG CCGGCGGGAG GTCGGGAGCT GTCGGACACG
801   CCGACGTGGG CGGTGGCGGT AGTCTGCGCC GTCATGATAC TCGTCTCCGT
851   CGCCATGGAG CACGCGCTCC ACAAGCTCGG CCACGTACGT GCTCTCGGTT
901   CACTAGTGCT TAACTGTTTT TGATGTTTTC GGGCGTGTTT GGTAGCCTGC
951   ATGGAGAGTG TATGAGCCCA AAAGTTCCCT CCCCGACCCA CTTTTCGCTG
1001  TTTGGTAGGG TGTATGGGCT GAGGAGAGCA TGCATCAACT GATGCAAAAA
1051  GGGCCTCAGC ATAGCTGAGC CCAGCACCCC CGCAGAGGCG AGCTGAGGCG
1101  AGTTATGCTG AGCCCATGCA CCCTCGCCCC GTCGCCCCGT CGCCCCGTCG
1151  CTCCCCCCCT GCACCTCTTC CTCCTCCCTC TTCCTACCAA ACACAGTCTC
1201  ATCCAAACAT GTAACAACAC ATGCATGACC ACCAAACAAC TGAAGATGAA
1251  TGTATTCATC ATGTCTATAC TTACCATGCA TCAACAGGGA ACAACTATGC
1301  TAGGGTGAGA ACAGCTGCCA AACACACCCG TGCACCTACT CATGCTGTGC
1351  CGGCGCTGGC GTACGTGTGC AGTGGTTCCA CAAGTGGCGC AAGAAGGCCC
1401  TGGGGGAGGC GCTGGAGAAG ATGAAGGCGG AGCTCATGCT GGTGGGCTTC
1451  ATATCCCTGC TCCTCATCGT CACGCAGGAT CCCGTCTCCA GGATCTGCAT
1501  CTCCAAGGAG GCCGGCGAGA AGATGCTCCC GTGCAAGCCT TACGACGGCG
1551  CCGGCGGTGG CAAAGGCAAG GACAATCACC GGAGGCTTCT CTGGCTCCAA
1601  GGCGAGAGCG AGACCCACCG CCGGTTCCTG GCTGCCCCGG CCGGAGTGGA
1651  CGTCTGCGCC AAACAGGTGA GCACCTAGCG TCGCCACAAA CCACAAACTA
1701 GCTAATGAGC ATGGACCTGA ATTTCTTCTC TTCTTGGCTT GGCTTGACTA
1751 AATTGGTTGT GCAGGGCAAG GTGGCGCTGA TGTCAGCGGG AAGCATGCAC
1801 CAACTGCACA TATTCATCTT CGTGCTCGCC GTCTTCCACG TCTTGTACAG
1851 CGTCGTCACC ATGACCCTAA GCCGTCTCAA AGTGAGCATC ATACTCGAGC
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1901 TGTTTGTCAA TAATCCTTGG TTTCCAATCC AATTCCAAAG CTGGCACTGA
1951 TCCTGCTCCG GCTTCCTGCA GATGAAGCAA TGGAAGAAGT GGGAGTCGGA
2001 GACCGCCTCG CTGGAGTATC AGTTCGCGAA TGGTCAGCTT CAACTTTTCT
2051 TACTGAAACC GGATGCATTT ACAACAAACG CACGCACGAT CAATCATCAC
2101 AGTGTGAGCC GATACGTTGA ACCGATTGAA TCCTCGCAGA TCCATCGCGG
2151 TGCCGGTTCA CGCACCAGAC GACGTTGGTG AGGCGGCACC TGGGCCTCTC
2201 CAGCACCCCC GGCGTCAGAT GGGTGGTGGC CTTCTTCAGG CAGTTCTTCA
2251 CGTCGGTGAC CAAGGTGGAC TACCTGACCT TGCGGCAGGG CTTCATCAAC
2301 GCGCATCTCT CGCAGGGCAA CAGGTTCGAC TTCCACAAGT ACATCAAGAG
2351 GTCGTTGGAG GACGACTTCA AGTCGTCGT CCGCATCAGG TACGCGCCAT
2401 TCCTTTCTCT GCACAAATTA ATACATCCAC CACCACATAG GTAGATAGAT
2451 AGATCGATAG ATAGATTATA CAAGTGCCGG TACGTACGTA CGTCTCATAT
2501 GATCTTGACA CATCTGTCCT CTTGCCGCAG TCTCAAGCTC TGGTTCGTGG
2551 CGGTCCTCAT CCTCTTCCTT GATTTCGACG GTAGCCGCCT TGTCCATGCC
2601 CTGCTCGCCC TCTCCTCCGC TTCTCTCCAT AATTTGTGAA CTTGTCCCGT
2651 ATATAACCAC ACCACCGTCG TCTTCTCGCA GGGATCGGCA CTCTTCTCTG
2701 GATGTCCGTG GTTCCTCTCG TGGTAAGTCC ACAATTTGAA TAGACAACCT
2751 GTCCAATTGT GATGTACAGT ACCTCCAAAC TTAATTAACA TGTCATTTGC
2801 TGATGTCTTG CGTGTAACAT TAGATCCTCT TGTGGGTTGG GACCAAGCTG
2851 GAGATGGTGA TCATGGAGAT GGCCCAGGAG ATCCATGACC GGGAGAGCGT
2901 CGTCAAGGGT GCTCCCGCCG TCGAGCCCAG CAACAAGTAC TTCTGGTTCA
2951 ACCGGCCTGA CTGGGTCCTC TTCCTCATGC ACCTCACACT CTTCCAGAAC
3001 GCGTTTCAGA TGGCTCATTT CGTGTGGACA GTGGTACGTA CAAGTACTTG
3051 TCACTTCACT TAGGCTAACT CCAACAAACG ACCCCAAATT AATGGTCCGT
3101 CGCGTCTGTT TGGGGTATGT TTGGGGTAAA CGGACACAAA ACTCAATCCA
3151 ACGCGCGGTA GCAAACGAAC GTTTTTCCGT ACGTTTTCGT CCGCTTTCGC
3201 CCCATCCCAG CCCAAATTCG TTGACGTTGT TGCATCGCAG GCCACGCCCG
3251 GCTTGAAGAA ATGCTACCAC GAGAAAATGG CAATGAGCAT CGCCAAGGTC
3301 GTGCTGGGGG TAGCCGCCCA GATCTTGTGC AGCTACATCA CCTTCCCGCT
3351 CTACGCGCTC GTCACGCAGA TGGGCTCACA CATGAAGAGA AGCATCTTCG
3401 ACGAGCAGAC GGCCAAGGCG CTGACCAACT GGCGAAAGAT GGCCAAGGAG
3451 AAGAAGAAGG CCCGAGACGC GGCCATGCTG ATGGCGCAGA TGGGCGGCGG
3501 CGCGACGCCG AGCGTCGGCT CGTCGCCGGT GCACCTGCTC CACAAGGCCG
3551 GGGCGCGGTC CGACGACCCC CAGAGCGTGC CGGCGTCCCC GAGGGCCGAG
3601 AAGGAAGGCG GCGGCGTGCA GCATCCGGCG CGCAAGGTAC CTCCTTGTGA
3651 CGGGTGGAGG TCGGCCTCGT CGCCGGCGCT CGACGCTCAC ATCCCCGGTG
3701 CAGATTTTGG CTTCAGCACG CAACGTTGAC CGATCAGACA AGTTCCTTTT
3751 TTTTTCGGTG AATAGAAGCG TATCATTTCA TTGATAGACA GTAGAAATTA
3801 CAGGAATGGC TGTCCTACTA CTATGTACAC AAGGGCACAG CAAAGGATCA
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SUBSTITUTE SHEET (RULE 26)

Figure 9 cont'd

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3851  TTGATCTTGT TACAAGAGCA GTAGAAAGGG ATTGCTCTCC ATTGATCTTG
3901  TTAAGTTGTA TGTCACAAAT TGTTGCAGAA AAAAGTGTAT GTCATCCCAA
3951  CCAAGAGCTG AGTTTGTGAT GATTCGTGCA ATAAGAATTG CAAGTTTCAC
4001  CGAGTCAAAA ATGAAGCTTC TAAGTACGCA CCAACCAACG GACTCTTTCA
4051  TCTCAACAAA AGAACTGTAA ATGGCAATAA TTCTGATAAC ATCGGAAGGG
4101  AGCTC
```

SUBSTITUTE SHEET (RULE 26)

Figure 10

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   1  ATGGCAGGTG GGAGATCGGC ATCGCGGGAG TTGCCGGAGA CGCCGACGTG
  51  GGCGGTGGCC GTCGTCTGCG CCGTCCTCGT GCTCGTCTCC GCCGCCATGG
 101  AGCACGGCCT CCACAACCTC AGCCATAAAA CCACCGCAGA AGTTCTCATA
 151  TTTCTTGTCC TATCTCCACT TGCAGAGCTG ATGCTGCTGG GCTTCATATC
 201  CCTGCTTCTC ACCGTGGCAC AGGCGCCCAT CTCCAAGATC TGCATCCCCA
 251  AGTCGGCTGC CAACATCTTG TTGCCGTGCA AGGCAGGCCA AGATGCCATC
 301  GAAGAAGAAG CAGCAAGTGG TCGCCGGTCC TTGGCCGGCG CCGGCGGCGG
 351  GGACTACTGC TCGAAATTCG ATGGCAAGGT GGCGCTGATG TCGGCAAAGA
 401  GCATGCACCA GCTGCACATT TTCATCTTCG TGCTCGCCGT GTTCCATGTT
 451  ACCTACTGCA TCATCACCAT GGGTTTAGGG CGCCTCAAAA TGAAGAAATG
 501  GAAGAAGTGG GAGTCACAGA CCAACTCATT GGAGTATCAG TTCGCAATCG
 551  ATCCTTCACG ATTCAGGTTC ACGCATCAGA CGTCGTTCGT GAAGCGGCAT
 601  CTGGGATCAT TCTCAAGCAC CCCTGGGCTC AGATGGATCG TAGCATTCTT
 651  CAGGCAGTTC TTTGGGTCCG TCACCAAGGT GGACTACCTG ACCATGCGGC
 701  AAGGCTTCAT CAATGCGCAT TTGTCGCAGA ATAGCAAGTT CGACTTCCAC
 751  AAATACATCA AGAGGTCTTT GGAGGACGAC TTCAAAGTTG TCGTTGGCAT
 801  CAGCCTCCCT CTGTGGTTCG TCGGAATCCT TGTACTCTTC CTCGATATCC
 851  ACGGTCTTGG CACACTTATT TGGATCTCTT TTGTTCCTCT CATCATCGTC
 901  TTGTTAGTTG GGACCAAGCT ACAGATGGTG ATCATGGAGA TGGCCCAAGA
 951  GATACAGGAC AGGGCCACTG TGATCCAGGG AGCACCTATG GTTGAACCAA
1001  GCAACAAGTA CTTCTGGTTC AACCGCCCTG ACTGGGTCTT GTTTTTCATA
1051  CACCTGACAC TCTTCCATAA CGCATTTCAG ATGGCGCATT TCGTATGGAC
1101  TATGGCAACA CCTGGTCTGA AGAAATGCTT CCATGAAAAT ATTTGGCTGA
1151  GCATCGTGGA AGTCATTGTG GGGATCTCTC TTCAGGTGCT ATGCAGCTAC
1201  ATCACCTTCC CGCTCTACGC GCTCGTCACA CAGATGGGAT CGAACATGAA
1251  GAAGACAATT TTCGAGGAGC AAACGATGAA GGCGCTGATG AACTGGAGGA
1301  AGAAGGCGAT GGAGAAGAAG AAGGTCCGGG ACGCCGACGC GTTCCTGGCG
1351  CAGATGAGCG TCGACTTCGC GACGCCGGCG TCGAGCCGGT CCGCGTCGCC
1401  GGTGCACCTG CTGCAGGTCA CAGGGCGGGT CGGACGCCCG CCGAGCCCAA
1451  TCACGGTGGC CTCACCACCG GCACCGGAGG AGGACATGTA CCCGGTGCCG
1501  GCGGCGGCTG CGTCTCGCCA GCTGCTAGAC GACCCGCCGG ACAGGAGGTG
1551  GATGGCATCC TCGTCGGCCG ACATCGCCGA TTCTGATTTT TCCTTCAGCG
1601  CACAACGGTG A
```

SUBSTITUTE SHEET (RULE 26)

Figure 11

```
   1  ATGGCTGGGC CGGCGGGAGG TCGGGAGCTG TCGGACACGC CGACGTGGGC
  51  GGTGGCGGTA GTCTGCGCCG TCATGATACT CGTCTCCGTC GCCATGGAGC
 101  ACGCGCTCCA CAAGCTCGGC CACTGGTTCC ACAAGTGGCG CAAGAAGGCC
 151  CTGGGGGAGG CGCTGGAGAA GATGAAGGCG GAGCTCATGC TGGTGGGCTT
 201  CATATCCCTG CTCCTCATCG TCACGCAGGA TCCCGTCTCC AGGATCTGCA
 251  TCTCCAAGGA GGCCGGCGAG AAGATGCTCC CGTGCAAGCC TTACGACGGC
 301  GCCGGCGGTG GCAAAGGCAA GGACAATCAC CGGAGGCTTC TCTGGCTCCA
 351  AGGCGAGAGC GAGACCCACC GCCGGTTCCT GGCTGCCCCG GCCGGAGTGG
 401  ACGTCTGCGC CAAACAGGGC AAGGTGGCGC TGATGTCAGC GGGAAGCATG
 451  CACCAACTGC ACATATTCAT CTTCGTGCTC GCCGTCTTCC ACGTCTTGTA
 501  CAGCGTCGTC ACCATGACCC TAAGCCGTCT CAAAATGAAG CAATGGAAGA
 551  AGTGGGAGTC GGAGACCGCC TCGCTGGAGT ATCAGTTCGC GAATGATCCA
 601  TCGCGGTGCC GCTTCACGCA CCAGACGACG TTGGTGAGGC GGCACCTGGG
 651  CCTCTCCAGC ACCCCCGGCG TCAGATGGGT GGTGGCCTTC TTCAGGCAGT
 701  TCTTCACGTC GGTGACCAAG GTGGACTACC TGACCTTGCG GCAGGGCTTC
 751  ATCAACGCGC ATCTCTCGCA GGGCAACAGG TTCGACTTCC ACAAGTACAT
 801  CAAGAGGTCG TTGGAGGACG ACTTCAAAGT CGTCGTCCGC ATCAGTCTCA
 851  AGCTCTGGTT CGTGGCGGTC CTCATCCTCT TCCTTGATTT CGACGGGATC
 901  GGCACTCTTC TCTGGATGTC CGTGGTTCCT CTCGTGATCC TCTTGTGGGT
 951  TGGGACCAAG CTGGAGATGG TGATCATGGA GATGGCCCAG GAGATCCATG
1001  ACCGGGAGAG CGTCGTCAAG GGTGCTCCCG CCGTCGAGCC CAGCAACAAG
1051  TACTTCTGGT TCAACCGGCC TGACTGGGTC CTCTTCCTCA TGCACCTCAC
1101  ACTCTTCCAG AACGCGTTTC AGATGGCTCA TTTCGTGTGG ACAGTGGCCA
1151  CGCCCGGCTT GAAGAAATGC TACCACGAGA AAATGGCAAT GAGCATCGCC
1201  AAGGTCGTGC TGGGGGTAGC CGCCCAGATC TTGTGCAGCT ACATCACCTT
1251  CCCGCTCTAC GCGCTCGTCA CGCAGATGGG CTCACACATG AAGAGAAGCA
1301  TCTTCGACGA GCAGACCGCC AAGGCGCTGA CCAACTGGCG AAAGATGGCC
1351  AAGGAGAAGA AGAAGGCCCG AGACGCGGCC ATGCTGATGG CGCAGATGGG
1401  CGGCGGCGCG ACGCCGAGCG TCGGCTCGTC GCCGGTGCAC CTGCTCCACA
1451  AGGCCGGGGC GCGCTCCGAC GACCCCCAGA GCGTGCCGGC GTCCCCGAGG
1501  GCCGAGAAGG AAGGCGGCGG CGTGCAGCAT CCGGCGCGCA AGGTACCTCC
1551  TTGTGACGCG TGGAGGTCGG CCTCGTCGCC GGCGCTCGAC GCTCACATCC
1601  CCGCTGCAGA TTTTGGCTTC AGCACGCAAC GTTGA
```

SUBSTITUTE SHEET (RULE 26)

```
1     GTTGGTACAT AAAAGACTCT TCCTTTGTCT GTTTTTTGTT CCCAGATTCA
51    TCTTTACTTA TTGACTAAAT TCTCTCTGGT GTGAGAAGTA AAATGGGTCA
101   CGGAGGAGAA GGGATGTCGC TTGAATTCAC TCCGACGTGG GTCGTCGCCG
151   GAGTTTGTAC GGTCATCGTC GCGATTTCAC TGGCGGTGGA GCGTTTGCTT
201   CACTATTTCG GTACTGTTCT TAAGAAGAAG AAGCAAAAAC CCCTTTACGA
251   AGCCCTTCAA AAGGTTAAAG AAGAGCTGAT GTTGTTAGGG TTTATATCGC
301   TGTTACTGAC GGTATTCCAA GGGCTCATTT CCAAATTCTG TGTGAAAGAA
351   AATGTGCTTA TGCATATGCT TCCATGTTCT CTCGATTCAA GACGAGAAGC
401   TGGGGCAAGT GAACATAAAA ACGTTACAGC AAAAGAACAT TTTCAGACTT
451   TTTTACCTAT TGTTGGAACC ACTAGGCGTC TACTTGCTGA ACATGCTGCT
501   GTGCAAGTTG GTTACTGTAG CGAAAAGGGT AAAGTACCAT TGCTTTCGCT
551   TGAGGCATTG CACCATCTAC ATATTTTCAT CTTCGTCCTC GCCATATCCC
601   ATGTGACATT CTGTGTCCTT ACCGTGATTT TTGGAAGCAC AAGGATTCAC
651   CAATGGAAGA AATGGGAGGA TTCGATCGCA GATGAGAAGT TTGACCCCGA
701   AACAGCTCTC AGGAAAAGAA GGGTCACTCA TGTACACAAC CATGCTTTTA
751   TTAAAGAGCA TTTTCTTGGT ATTGGCAAAG ATTCAGTCAT CCTCGGATGG
801   ACGCAATCCT TTCTCAAGCA ATTCTATGAT TCTGTGACGA AATCAGATTA
851   CGTGACTTTA CGTCTTGGTT TCATTATGAC ACATTGTAAG GGAAACCCCA
901   AGCTTAATTT CCACAAGTAT ATGATGCGCG CTCTAGAGGA TGATTTCAAA
951   CAAGTTGTTG GTATTAGTTG GTATCTTTGG ATCTTTGTCG TCATCTTTTT
1001  GCTGCTAAAT GTTAACGGAT GGCACACATA TTTCTGGATA GCATTTATTC
1051  CCTTTGCTTT GCTTCTTGCT GTGGGAACAA AGTTGGAGCA TGTGATTGCA
1101  CAGTTAGCTC ATGAAGTTGC AGAGAAACAT GTAGCCATTG AAGGAGACTT
1151  AGTGGTGAAA CCCTCAGATG AGCATTTCTG GTTCAGCAAA CCTCAAATTG
1201  TTCTCTACTT GATCCATTTT ATCCTCTTCC AGAATGCTTT TGAGATTGCG
1251  TTTTTCTTTT GGATTTGGGT TACATACGGC TTCGACTCGT GCATTATGGG
1301  ACAGGTGAGA TACATTGTTC CAAGATTGGT TATCGGGGTC TTCATTCAAG
1351  TGCTTTGCAG TTACAGTACA CTGCCTCTTT ACGCCATCGT CTCACAGATG
1401  GGAAGTAGCT TCAAGAAAGC TATATTCGAG GAGAATGTGC AGGTTGGTCT
1451  TGTTNGTTGG GCACAGAAAG TGAAACAAAA GAGAGACCTA AAAGCTGCAG
1501  CTAGTAATGG AGACGAAGGA AGCTCTCAGG CTGGTCCTGG TCCTGATTCT
1551  GGTTCTGGTT CTGCTCCTGC TGCTGGTCCT GGTGCAGGTT TTGCAGGAAT
1601  TCAGCTCAGC AGAGTAACAA GAAACAACGC AGGGGACACA AACAATGAGA
1651  TTACACCTGA TCATAACAAC TGAGCAGAGA TATTATCTTT TCCATTTAGA
1701  GGATCATCAT CAGATTTTAG CTTCAAGGTC CGGTTTTGTG GTTTATACAT
1751  AAGTTATAGT GACTTGATTT TTTTGTTTTG TTACAAAGTT ACCATCTTTG
1801  GATTAGAATT GGGAAATTGA ATCTGTTTGT ATATTGTATT ATTTGGAACA
1851  TTGTGGATGC CCATGGATAT GTTTCTGTTC
```

SUBSTITUTE SHEET (RULE 26)

```
1   MAGGRSGSRE LPETPTWAVA VVCAVLVLVS AAMEHGLHNL SHKTTAEVLI
51  FLVLSALAEL MLLGFISLLL TVAQAPISKI CIPKSAANIL LPCKAGQDAI
101 EEEAASGRRS LAGAGGGDYC SKFDGKVALM SAKSMHQLHI FIFVLAVFHV
151 TYCIITMGLG RLKMKKWKKW ESQTNSLEYQ FAIDPSRFRF THQTSFVKRH
201 LGSFSSTPGL RWIVAFFRQF FGSVTKVDYL TMRQGFINAH LSQNSKFDFH
251 KYIKRSLEDD FKVVVGISLP LWFVGILVLF LDIHGLGTLI WISFVPLIIV
301 LLVGTKLEMV IMEMAQEIQD RATVIQGAPM VEPSNKYFWF NRPDWVLFFI
351 HLTLFHNAFQ MAHFVWTMAT PGLKKCFHEN IWLSIVEVIV GISLQVLCSY
401 ITFPLYALVT QMGSNMKKTI FEEQTMKALM NWRKKAMEKK KVRDADAFLA
451 QMSVDFATPA SSRSASPVHL LQVTGRVGRP PSPITVASPP APEEDMYPVP
501 AAAASRQLLD DPPDRRWMAS SSADIADSDF SFSAQR*
```

SUBSTITUTE SHEET (RULE 26)

```
1   MAGPAGGREL SDTPTWAVAV VCAVMILVSV AMEHALHKLG HWFHKWRKKA
51  LGEALEKMKA ELMLVGFISL LLIVTQDPVS RICISKEAGE KMLPCKPYDG
101 AGGGKGKDNH RRLLWLQGES ETHRRFLAAP AGVDVCAKQG KVALMSAGSM
151 HQLHIFIFVL AVFHVLYSVV TMTLSRLKMK QWKKWESETA SLEYQFANDP
201 SRCRFTHQTT LVRRHLGLSS TPGVRWVVAF FRQFFTSVTK VDYLTLRQGF
251 INAHLSQGNR FDFHKYIKRS LEDDFKVVVR ISLKLWFVAV LILFLDFDGI
301 GTLLWMSVVP LVILLWVGTK LEMVIMEMAQ EIHDRESVVK GAPAVEPSNK
351 YFWFNRPDWV LFLMHLTLFQ NAFQMAHFVW TVATPGLKKC YHEKMAMSIA
401 KVVLGVAAQI LCSYITFPLY ALVTQMGSHM KRSIFDEQTA KALTNWRKMA
451 KEKKKARDAA MLMAQMGGGA TPSVGSSPVH LLHKAGARSD DPQSVPASPR
501 AEKEGGGVQH PARKVPPCDG WRSASSPALD AHIPGADFGF STQR*
```

SUBSTITUTE SHEET (RULE 26)

Figure 15

SUBSTITUTE SHEET (RULE 26)

```
  1  MGHGGSGMSL EFTPTWVVAG VCTVIVAISL AVERLLHYFG TVLKKKKQKP
 51  LYEALQKVKE ELMLLGFISL LLTVFQGLIS KFCVKENVLM HMLPCSLDSR
101  REAGASEHKN VTAKEHFQTP LPIVGTTRRL LAEHAAVQVG YCSEKGKVPL
151  LSLEALHHLH IFIFVLAISH VTFCVLTVIF GSTRIHQWKK WEDSIADEKF
201  DPETALRKRR VTHVHNHAFI KEHFLGIGKD SVILGWTQSF LKQFYDSVTK
251  SDYVTLRLGF IMTHCKGNPK LNFHKYMMRA LEDDFKQVVG ISWYLWIFVV
301  IFLLLNVNGW HTYFWIAFIP FALLLAVGTK LEHVIAQLAH EVAEKHVAIF
351  GDLVVKPSDE HFWFSKPQIV LYLIHFILFQ NAFEIAFFFW IWVTYGFDSC
401  IMGQVRYIVP RLVIGVFIQV LCSYSTLPLY AIVSQMGSSF KKAILEENVQ
451  VGLVGWAQKV KQKRDLKAAA SNGDEGSSQA GPGPDSGSGS APAAGPGAGF
501  AGIQLSRVTR NNAGDTNNEI TPDHNN*
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SUBSTITUTE SHEET (RULE 26)

FIGURE 16

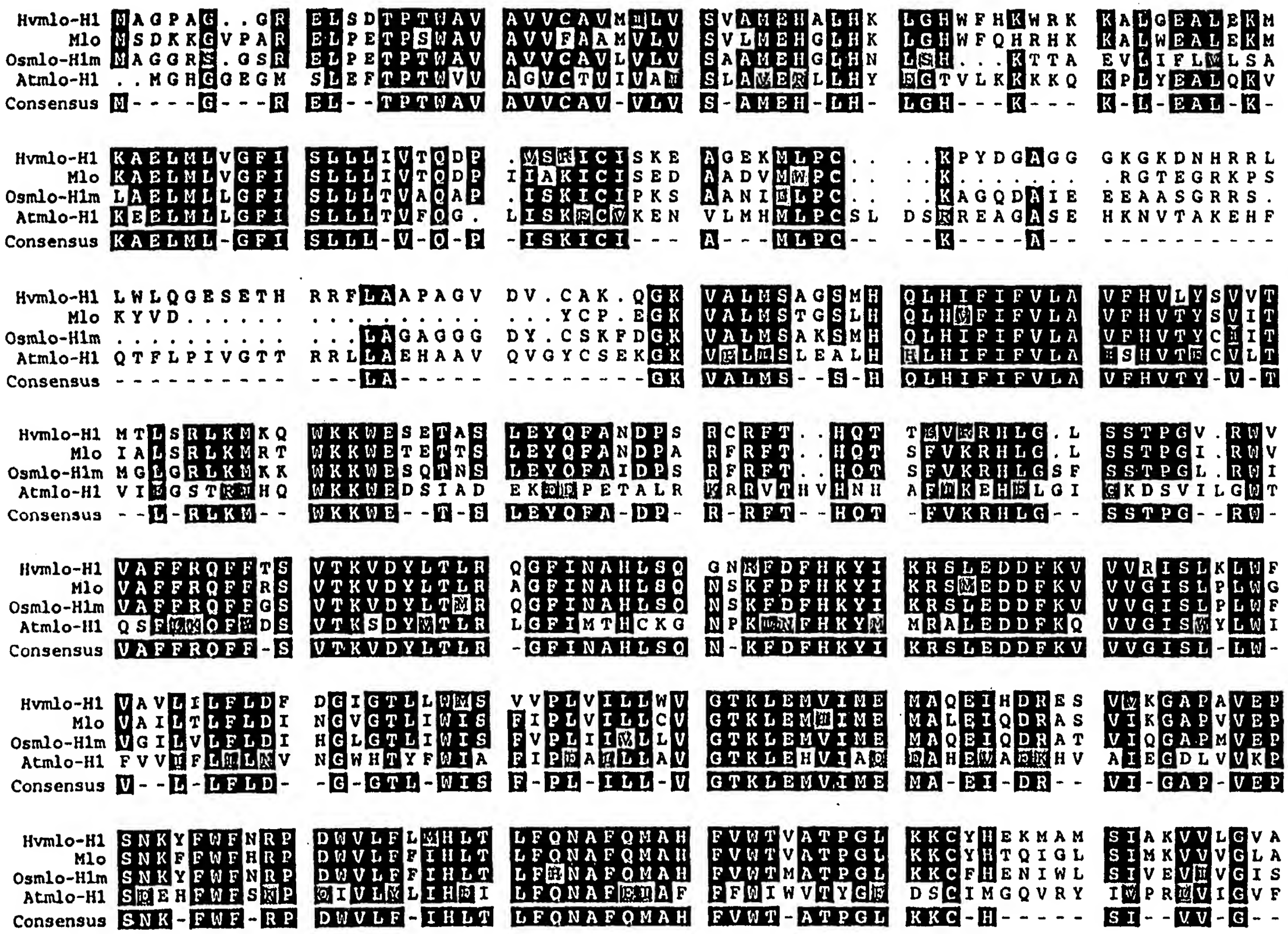

FIGURE 16 (CONT/D)

```
Hvmlo-H1  AQILCSYITF  PLYALVTQMG  SHMKRSIFDE  QTAKALTNWR  KMAKEKKKAR  DAAMLMAQMG
    Mlo   LQFLCSYMTF  PLYALVTQMG  SNMKRSIFDE  QTSKALTNWR  NTAKEKKKVR  DTDMLMAQMI
Osmlo-H1m LQVLCSYITF  PLYALVTQMG  SNMKKTIFEE  QTMKALMNWR  KKAMEKKKVR  DADAFLAQMS
 Atmlo-H1 IQVLCSYSTE  PLYAEVSQMG  SSFKKAIFEE  NVQVGLVGWA  QKVKQKRDLK  AAASNGDEGS
Consensus -Q-LCSY-TF  PLYALVTQMG  S-MK--IF-E  QT-KAL-NWR  --AKEKKK-R  DA----AQM-

Hvmlo-H1  GGATPSVGSSPV  HLLHKAGARS  DDPQSVPASP  RAEKEG....  .GGVQHPARK
    Mlo   GDATPSRGSSPV  HLLHKGMGRS  DDPQSAPTSP  RTQQEARDMY  PVVVAHPVHR
Osmlo-H1m VD.....FAT  PASSRSASPV  HLLQ.VTGRV  GRPPSPITVA  SPPAPEEDMY  PVPAAAASRQ
 Atmlo-H1 SQAGPGPDSG  SGSAPAAGP.  .....GAGFA  GIQLSRVTRN  NAGDTNNEIT  PDHNN*....
Consensus --A-------  ---S---SPV  HLL----GR-  --P-S--T--  ----------  P---------

Hvmlo-H1  V..PPCDGWR  SASSPALDAH  IPGADFGFST  QR*
    Mlo   L..NPNDRRR  SASSSALEAD  IPSADFSFSQ  G*.
Osmlo-H1m LLDDPPDRRW  MASSS...AD  IADSDFSFSA  QR*
 Atmlo-H1 ..........  ..........  ..........  ...
Consensus ----P-D---  -ASS----A-  I---DF-FS-  ---
```

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